desired remodeled glycan structure. Figure 40G are the formulas for the glycans that bind to the N-linked glycosylation sites (A and A') and to the O-linked sites (B) of the Factor VIII peptides. Figure 40H to 40M are diagrams of contemplated remodeling steps of the peptides in Figure 40G based on the type of cell the peptide is expressed in and the desired remodeled

5   glycan structures.

Figure 41, comprising Figures 41A to 41M, sets forth exemplary schemes for remodeling glycan structures on urokinase. Figure 41A is a diagram depicting the urokinase peptide indicating a residue which binds to a glycan contemplated for remodeling, and an exemplary glycan formula bound thereto. Figure 41B to 41G are diagrams of contemplated

10   remodeling steps of the peptide in Figure 41A based on the type of cell the peptide is expressed in and the desired remodeled glycan structure. Figure 41H is a diagram depicting the urokinase peptide indicating a residue which binds to a glycan contemplated for remodeling, and an exemplary glycan formula bound thereto. Figure 41I to 41M are diagrams of contemplated remodeling steps of the peptide in Figure 41H based on the type of

15   cell the peptide is expressed in and the desired remodeled glycan structure.

Figure 42, comprising Figures 42A to 42K, sets forth exemplary schemes for remodeling glycan structures on human DNase (hDNase). Figure 42A is a diagram depicting the human DNase peptide indicating the residues which bind to glycans contemplated for remodeling, and exemplary glycan formulas bound thereto. Figure 42B to 42G are diagrams

20   of contemplated remodeling steps of the peptide in Figure 42A based on the type of cell the peptide is expressed in and the desired remodeled glycan structure. Figure 42H is a diagram depicting the human DNase peptide indicating residues which bind to glycans contemplated for remodeling, and exemplary glycan formulas bound thereto. Figure 42I to 42K are diagrams of contemplated remodeling steps of the peptide in Figure 42H based on the type of

25   cell the peptide is expressed in and the desired remodeled glycan structure.

Figure 43, comprising Figures 43A to 43L, sets forth exemplary schemes for remodeling glycan structures on insulin. Figure 43A is a diagram depicting the insulin peptide mutated to contain an N glycosylation site and an exemplary glycan formula bound thereto. Figure 43B to 43D are diagrams of contemplated remodeling steps of the peptide in

30   Figure INS A based on the type of cell the peptide is expressed in and the desired remodeled glycan structure. Figure 43E is a diagram depicting insulin-mucin fusion peptides indicating

a residue(s) which binds to a glycan contemplated for remodeling, and an exemplary glycan formula bound thereto. Figure 43F to 43H are diagrams of contemplated remodeling steps of the peptide in Figure 43E based on the type of cell the peptide is expressed in and the desired remodeled glycan structure. Figure 43I is a diagram depicting the insulin-mucin fusion

5 peptides and insulin peptides indicating a residue(s) which binds to a glycan contemplated for remodeling, and formulas for the glycan. Figure 43J to 43L are diagrams of contemplated remodeling steps of the peptide in Figure 43I based on the type of cell the peptide is expressed in and the desired remodeled glycan structure.

Figure 44, comprising Figures 44A to 44K, sets forth exemplary schemes for

10 remodeling glycan structures on the M-antigen (preS and S) of the Hepatitis B surface protein (HbsAg). Figure 44A is a diagram depicting the M-antigen peptide indicating the residues which bind to glycans contemplated for remodeling, and formulas for the glycans. Figure 44B to 44G are diagrams of contemplated remodeling steps of the peptide in Figure 44A based on the type of cell the peptide is expressed in and the desired remodeled glycan

15 structure. Figure 44H is a diagram depicting the M-antigen peptide indicating the residues which bind to glycans contemplated for remodeling, and formulas for the glycans. Figure 44I to 44K are diagrams of contemplated remodeling steps of the peptide in Figure 44H based on the type of cell the peptide is expressed in and the desired remodeled glycan structure.

Figure 45, comprising Figures 45A to 45K, sets forth exemplary schemes for

20 remodeling glycan structures on human growth hormone, including N, V and variants thereof. Figure 45A is a diagram depicting the human growth hormone peptide indicating a residue which binds to a glycan contemplated for remodeling, and an exemplary glycan formula bound thereto. Figure 45B to 45D are diagrams of contemplated remodeling steps of the glycan of the peptide in Figure 45A based on the type of cell the peptide is expressed in

25 and the desired remodeled glycan structure. Figure 45E is a diagram depicting the three fusion peptides comprising the human growth hormone peptide and part or all of a mucin peptide, and indicating a residue(s) which binds to a glycan contemplated for remodeling, and exemplary glycan formula(s) bound thereto. Figure 45F to 45K are diagrams of contemplated remodeling steps of the glycan of the peptides in Figure 45E based on the type

30 of cell the peptide is expressed in and the desired remodeled glycan structure.

Figure 46, comprising Figures 46A to 46G, sets forth exemplary schemes for remodeling glycan structures on a TNF Receptor-IgG Fc region fusion protein (Enbrel™). Figure 46A is a diagram depicting a TNF Receptor--IgG Fc region fusion peptide which may be mutated to contain additional N-glycosylation sites indicating the residues which bind to

5   glycans contemplated for remodeling, and formulas for the glycans. The TNF receptor peptide is depicted in bold line, and the IgG Fc regions is depicted in regular line. Figure 46B to 46G are diagrams of contemplated remodeling steps of the peptide in Figure 46A based on the type of cell the peptide is expressed in and the desired remodeled glycan structure.

10 Figure 47 provides exemplary schemes for remodeling glycan structures on an anti-HER2 monoclonal antibody (Herceptin™). Figure 47A is a diagram depicting an anti-HER2 monoclonal antibody which has been mutated to contain an N-glycosylation site(s) indicating a residue(s) on the antibody heavy chain which binds to a glycan contemplated for remodeling, and an exemplary glycan formula bound thereto. Figure 47B to 47D are

15 diagrams of contemplated remodeling steps of the glycan of the peptides in Figure 47A based on the type of cell the peptide is expressed in and the desired remodeled glycan structure.

Figure 48, comprising Figures 48A to 48D, sets forth exemplary schemes for remodeling glycan structures on a monoclonal antibody to Protein F of Respiratory Syncytial Virus (Synagis™). Figure 48A is a diagram depicting a monoclonal antibody to Protein F

20 peptide which is mutated to contain an N-glycosylation site(s) indicating a residue(s) which binds to a glycan contemplated for remodeling, and an exemplary glycan formula bound thereto. Figure 48B to 48D are diagrams of contemplated remodeling steps of the peptide in Figure 48A based on the type of cell the peptide is expressed in and the desired remodeled glycan structure.

25 Figure 49, comprising Figures 49A to 49D, sets forth exemplary schemes for remodeling glycan structures on a monoclonal antibody to TNF-α (Remicade™). Figure 49A is a diagram depicting a monoclonal antibody to TNF-α which has been mutated to contain an N-glycosylation site(s) indicating a residue which binds to a glycan contemplated for remodeling, and an exemplary glycan formula bound thereto. Figure 49B to 49D are

30 diagrams of contemplated remodeling steps of the peptide in Figure 49A based on the type of cell the peptide is expressed in and the desired remodeled glycan structure.

Figure 50, comprising Figures 50A to 50D, sets forth exemplary schemes for remodeling glycan structures on a monoclonal antibody to glycoprotein IIb/IIIa (Reopro™). Figure 50A is a diagram depicting a mutant monoclonal antibody to glycoprotein IIb/IIIa peptides which have been mutated to contain an N-glycosylation site(s) indicating the

5   residue(s) which bind to glycans contemplated for remodeling, and exemplary glycan formulas bound thereto. Figure 50B to 50D are diagrams of contemplated remodeling steps based on the type of cell the peptide is expressed in and the desired remodeled glycan structure. Figure 50E is a diagram depicting monoclonal antibody to glycoprotein IIb/IIIa-mucin fusion peptides indicating the residues which bind to glycans contemplated for

10   remodeling, and exemplary glycan formulas bound thereto. Figure 50F to 50H are diagrams of contemplated remodeling steps based on the type of cell the peptide is expressed in and the desired remodeled glycan structure. Figure 50I is a diagram depicting monoclonal antibody to glycoprotein IIb/IIIa- mucin fusion peptides and monoclonal antibody to glycoprotein IIb/IIIa peptides indicating the residues which bind to glycans contemplated for remodeling,

15   and exemplary glycan formulas bound thereto. Figure 50J to 50L are diagrams of contemplated remodeling steps based on the type of cell the peptide is expressed in and the desired remodeled glycan structure.

Figure 51, comprising Figures 51A to 51D, sets forth exemplary schemes for remodeling glycan structures on a monoclonal antibody to CD20 (Rituxan™). Figure 51A is

20   a diagram depicting monoclonal antibody to CD20 which have been mutated to contain an N-glycosylation site(s) indicating the residue which binds to glycans contemplated for remodeling, and exemplary glycan formulas bound thereto. Figure 51B to 51D are diagrams of contemplated remodeling steps of the glycan of the peptides in Figure 51A based on the type of cell the peptide is expressed in and the desired remodeled glycan structure. Figure

25   51E is a diagram depicting monoclonal antibody to CD20 which has been mutated to contain an N-glycosylation site(s) indicating the residue(s) which binds to glycans contemplated for remodeling, and exemplary glycan formulas bound thereto. Figure 51F to 51G are diagrams of contemplated remodeling steps of the glycan of the peptides in Figure 51E based on the type of cell the peptide is expressed in and the desired remodeled glycan structure.

Figure 52, comprising Figures 51A and 51B, is an exemplary nucleotide and corresponding amino acid sequence of granulocyte colony stimulating factor (G-CSF) (SEQ ID NOS:1 and 2, respectively).

Figure 53, comprising Figures 53A and 53B, is an exemplary nucleotide and

5 corresponding amino acid sequence of interferon alpha (IFN-alpha) (SEQ ID NOS:3 and 4, respectively).

Figure 54, comprising Figures 54A and 54B, is an exemplary nucleotide and corresponding amino acid sequence of interferon beta (IFN-beta) (SEQ ID NOS:5 and 6, respectively).

10 Figure 55, comprising Figures 55A and 55B, is an exemplary nucleotide and corresponding amino acid sequence of Factor VIIa (SEQ ID NOS:7 and 8, respectively).

Figure 56, comprising Figures 56A and 56B, is an exemplary nucleotide and corresponding amino acid sequence of Factor IX (SEQ ID NOS:9 and 10, respectively).

Figure 57, comprising Figures 57A through 57D, is an exemplary nucleotide and

15 corresponding amino acid sequence of the alpha and beta chains of follicle stimulating hormone (FSH), respectively (SEQ ID NOS:11 through 14, respectively).

Figure 58, comprising Figures 58A and 58B, is an exemplary nucleotide and corresponding amino acid sequence of erythropoietin (EPO) (SEQ ID NOS:15 and 16, respectively).

20 Figure 59, comprising Figures 59A and 59B, is an exemplary nucleotide and corresponding amino acid sequence of granulocyte-macrophage colony stimulating factor (GM-CSF) (SEQ ID NOS:17 and 18, respectively).

Figure 60, comprising Figures 60A and 60B, is an exemplary nucleotide and corresponding amino acid sequence of interferon gamma (IFN-gamma) (SEQ ID NOS:19 and

25 20, respectively).

Figure 61, comprising Figures 61A and 61B, is an exemplary nucleotide and corresponding amino acid sequence of α-1-protease inhibitor (A-1-PI, or α-antitrypsin) (SEQ ID NOS:21 and 22, respectively).

Figure 62, comprising Figures 62A-1 to 62A-2, and 62B, is an exemplary nucleotide

30 and corresponding amino acid sequence of glucocerebrosidase (SEQ ID NOS:23 and 24, respectively).

Figure 63, comprising Figures 63A and 63B, is an exemplary nucleotide and corresponding amino acid sequence of tissue-type plasminogen activator (TPA) (SEQ ID NOS:25 and 26, respectively).

Figure 64, comprising Figures 64A and 64B, is an exemplary nucleotide and corresponding amino acid sequence of interleukin-2 (IL-2) (SEQ ID NOS:27 and 28, respectively).

Figure 65, comprising Figures 65A-1 through 65A-4 and Figure 65B-1 through 65B-4, is an exemplary nucleotide and corresponding amino acid sequence of Factor VIII (SEQ ID NOS:29 and 30, respectively).

Figure 66, comprising Figures 66A and 66B, is an exemplary nucleotide and corresponding amino acid sequence of urokinase (SEQ ID NOS:33 and 34, respectively).

Figure 67, comprising Figures 67A and 67B, is an exemplary nucleotide and corresponding amino acid sequence of human recombinant DNase (hrDNase) (SEQ ID NOS:39 and 40, respectively).

Figure 68, comprising Figures 68A and 68B, is an exemplary nucleotide and corresponding amino acid sequence of a humanized monoclonal antibody to glycoprotein IIb/IIIa (SEQ ID NOS:43 and 44, respectively).

Figure 69, comprising Figures 69A and 69B, is an exemplary nucleotide and corresponding amino acid sequence of S-protein from a Hepatitis B virus (HbsAg) (SEQ ID NOS:45 and 46, respectively).

Figure 70, comprising Figures 70A and 70B, is an exemplary nucleotide and corresponding amino acid sequence of human growth hormone (HGH) (SEQ ID NOS:47 and 48, respectively).

Figure 71, comprising Figures 71A and 71B, is an exemplary nucleotide and corresponding amino acid sequence of the 75 kDa tumor necrosis factor receptor (TNF-R), which comprises a portion of Enbrel™ (tumor necrosis factor receptor (TNF-R)/IgG fusion) (SEQ ID NOS:31 and 32, respectively).

Figure 72, comprising Figures 72A and 72B, is an exemplary amino acid sequence of the light and heavy chains, respectively, of Herceptin™ (monoclonal antibody (MAb) to Her-2, human epidermal growth factor receptor) (SEQ ID NOS:35 and 36, respectively).

Figure 73, comprising Figures 73A and 73B, is an exemplary amino acid sequence the heavy and light chains, respectively, of Synagis™ (MAb to F peptide of Respiratory Syncytial Virus) (SEQ ID NOS:37 and 38, respectively).

5   Figure 74, comprising Figures 74A and 74B, is an exemplary nucleotide and corresponding amino acid sequence of the non-human variable regions of Remicade™ (MAb to TNFα) (SEQ ID NOS:41 and 42, respectively).

Figure 75, comprising Figures 75A and 75B, is an exemplary nucleotide and corresponding amino acid sequence of the Fc portion of human IgG (SEQ ID NOS:49 and 50, respectively).

10   Figure 76 is an exemplary amino acid sequence of the mature variable region light chain of an anti-glycoprotein IIb/IIIa murine antibody (SEQ ID NO:52).

Figure 77 is an exemplary amino acid sequence of the mature variable region heavy chain of an anti-glycoprotein IIb/IIIa murine antibody (SEQ ID NO:54).

Figure 78 is an exemplary amino acid sequence of variable region light chain of a

15 human IgG (SEQ ID NO:51).

Figure 79 is an exemplary amino acid sequence of variable region heavy chain of a human IgG (SEQ ID NO:53).

Figure 80 is an exemplary amino acid sequence of a light chain of a human IgG (SEQ ID NO:55).

20   Figure 81 is an exemplary amino acid sequence of a heavy chain of a human IgG (SEQ ID NOS:56).

Figure 82, comprising Figures 82A and 82B, is an exemplary nucleotide and corresponding amino acid sequence of the mature variable region of the light chain of an anti-CD20 murine antibody (SEQ ID NOS:59 and 60, respectively).

25   Figure 83, comprising Figures 83A and 83B, is an exemplary nucleotide and corresponding amino acid sequence of the mature variable region of the heavy chain of an anti-CD20 murine antibody (SEQ ID NOS:61 and 62, respectively).

Figure 84, comprising Figures 84A through 84E, is the nucleotide sequence of the tandem chimeric antibody expression vector TCAE 8 (SEQ ID NOS:57).

Figure 85, comprising Figures 85A through 85E, is the nucleotide sequence of the tandem chimeric antibody expression vector TCAE 8 containing the light and heavy variable domains of the anti-CD20 murine antibody (SEQ ID NOS:58).

Figure 86 is an image of an acrylamide gel depicting the results of FACE analysis of the pre- and post-sialylation of TP10. The $BiNA_0$ species has no sialic acid residues. The $BiNA_1$ species has one sialic acid residue. The $BiNA_2$ species has two sialic acid residues. Bi = biantennary; NA = neuraminic acid.

Figure 87 is a graph depicting the plasma concentration in µg/ml over time of pre- and post-sialylation TP10 injected into rats.

Figure 88 is a graph depicting the area under the plasma concentration-time curve (AUC) in µg/hr/ml for pre- and post sialylated TP10.

Figure 89 is an image of an acrylamide gel depicting the results of FACE analysis of the pre- and post-fucosylation of TP10. The $BiNA_2F_2$ species has two neuraminic acid (NA) residues and two fucose residues (F).

Figure 90 is a graph depicting the *in vitro* binding of TP20 ($sCR1sLe^X$) glycosylated *in vitro* (diamonds) and *in vivo* in Lec11 CHO cells (squares).

Figure 91 is a graph depicting the analysis by 2-AA HPLC of glycoforms from the GlcNAc-ylation of EPO.

Figure 92, comprising Figures 92A and 92B, is two graphs depicting the MALDI-TOF spectrum of RNaseB (Figure 92A) and the HPLC profile of the oligosaccharides cleaved from RNaseB by N-Glycanase (Figure 92B). The majority of N-glycosylation sites of the peptide are modified with high mannose oligosaccharides consisting of 5 to 9 mannose residues.

Figure 93 is a scheme depicting the conversion of high mannose N-Glycans to hybrid N-Glycans. Enzyme 1 is α1,2-mannosidase, from *Trichodoma reesei* or *Aspergillus saitoi*. Enzyme 2 is GnT-I (β-1,2-*N*-acetyl glucosaminyl transferase I). Enzyme 3 is GalT-I (β1,4-galactosyltransfease 1). Enzyme 4 is α2,3-sialyltransferase or α2,6-sialyltransferase.

Figure 94, comprising Figures 94A and 94B, is two graphs depicting the MALDI-TOF spectrum of RNaseB treated with a recombinant *T. reesei* α1,2-mannosidase (Figure

94A) and the HPLC profile of the oligosaccharides cleaved by N-Glycanase from the modified RNaseB (Figure 94B).

Figure 95 is a graph depicting the MALDI-TOF spectrum of RNaseB treated with a commercially available α1,2-mannosidase purified from *A. saitoi* (Glyko & CalBioChem).

5   Figure 96 is a graph depicting the MALDI-TOF spectrum of modified RNaseB by treating the product shown in Figure 94 with a recombinant GnT-I (GlcNAc transferase-I).

Figure 97 is a graph depicting the MALDI-TOF spectrum of modified RNaseB by treating the product shown in Figure 96 with a recombinant GalT 1 (galactosyltransferase 1).

Figure 98 is a graph depicting the MALDI-TOF spectrum of modified RNaseB by

10   treating the product shown in Figure 97 with a recombinant ST3Gal III (α2,3-sialyltransferase III) using CMP-SA as the donor for the transferase.

Figure 99 is a graph depicting the MALDI-TOF spectrum of modified RNaseB by treating the product shown in Figure 97 with a recombinant ST3Gal III (α2,3-sialyltransferase III) using CMP-SA-PEG (10 kDa) as the donor for the transferase.

15   Figure 100 is a series of schemes depicting the conversion of high mannose N-glycans to complex N-glycans. Enzyme 1 is α1,2-mannosidase from *Trichoderma reesei* or *Aspergillus saitoi*. Enzyme 2 is GnT-I. Enzyme 3 is GalT 1. Enzyme 4 is α2,3-sialyltransferase or α2,6-sialyltransferase. Enzyme 5 is α-mannosidase II. Enzyme 6 is α-mannosidase. Enzyme 7 is GnT-II. Enzyme 8 is α1,6-mannosidase. Enzyme 9 is α1,3-

20   mannosidase.

Figure 101 is a diagram of the linkage catalyzed by *N*-acetylglucosaminyltransferase I to VI (GnT I-VI). R = GlcNAcβ1,4GlcNAc-Asn-X.

Figure 102, comprising Figures 102A and 102B, are graphs depicting the 2-AA HPLC analysis of two lots of EPO to which N-acetylglucosamine was been added. Figure 102A

25   depicts the analysis of lot A, and Figure 102B depicts the analysis of lot B.

Figure 103 is a graph depicting the 2-AA HPLC analysis of the products the reaction introducing a third glycan branch to EPO with GnT-V.

Figure 104 is a graph depicting a MALDI-TOF spectrum of the glycans of the EPO preparation after treatment with GnT-I, GnT-II, GnT-III, GnT-IV and GalT1, with

30   appropriate donor groups.

Figure 105 is an image of an isoelectric focusing (IEF) gel depicting the products of the desialylation reaction of human pituitary FSH. Lanes 1 and 4 are isoelectric focusing (IEF) standards. Lane 2 is native FSH. Lane 3 is desialylated FSH.

Figure 106 is an image of an SDS-PAGE gel of the products of the reactions to make
5   PEG-sialylation of rFSH. Lanes 1 and 8 are SeeBlue+2 molecular weight standards. Lane 2 is 15 μg of native FSH. Lane 3 is 15 μg of asialo-FSH (AS-FSH). Lane 4 is 15 μg of the products of the reaction of AS-FSH with CMP-SA. Lane 5 is 15 μg of the products of the reaction of AS-FSH with CMP-SA-PEG (1kDa). Lane 6 is 15 μg of the products of the reaction of AS-FSH with CMP-SA-PEG (5kDa). Lane 7 is 15 μg of the products of the
10   reaction of AS-FSH with CMP-SA-PEG (10 kDa).

Figure 107 is an image of an isoelectric focusing gel of the products of the reactions to make PEG-sialylation of FSH. Lanes 1 and 8 are IEF standards. Lane 2 is 15 μg of native FSH. Lane 3 is 15 μg of asialo-FSH (AS-FSH). Lane 4 is 15 μg of the products of the reaction of AS-FSH with CMP-SA. Lane 5 is 15 μg of the products of the reaction of AS-
15   FSH with CMP-SA-PEG (1kDa). Lane 6 is 15 μg of the products of the reaction of AS-FSH with CMP-SA-PEG (5kDa). Lane 7 is 15 μg of the products of the reaction of AS-FSH with CMP-SA-PEG (10 kDa).

Figure 108 is an image of an SDS-PAGE gel of native non-recombinant FSH produced in human pituitary cells. Lanes 1, 2 and 5 are SeeBlue™+2 molecular weight
20   standards. Lanes 3 and 4 are native FSH at 5 μg and 25 μg, respectively.

Figure 109 is an image of an isoelectric focusing gel (pH 3-7) depicting the products of the asialylation reaction of rFSH. Lanes 1 and 4 are IEF standards. Lane 2 is native rFSH. Lane 3 is asialo-rFSH.

Figure 110 is an image of an SDS-PAGE gel depicting the results of the PEG-
25   sialylation of asialo-rFSH. Lane 1 is native rFSH. Lane 2 is asialo-FSH. Lane 3 is the products of the reaction of asialo-FSH and CMP-SA. Lanes 4-7 are the products of the reaction between asialoFSH and 0.5 mM CMP-SA-PEG (10 kDa) at 2 hr, 5 hr, 24 hr, and 48 hr, respectively. Lane 8 is the products of the reaction between asialo-FSH and 1.0 mM CMP-SA-PEG (10 kDa) at 48 hr. Lane 9 is the products of the reaction between asialo-FSH
30   and 1.0 mM CMP-SA-PEG (1 kDa) at 48 hr.

Figure 111 is an image of an isoelectric focusing gel showing the products of PEG-sialylation of asialo-rFSH with a CMP-SA-PEG (1 kDa). Lane 1 is native rFSH. Lane 2 is asialo-rFSH. Lane 3 is the products of the reaction of asialo-rFSH and CMP-SA at 24 hr. Lanes 4-7 are the products of the reaction of asialo-rFSH and 0.5 mM CMP-SA-PEG (1 kDa)

5   at 2 hr, 5 hr, 24 hr, and 48 hr, respectively. Lane 8 is blank. Lanes 9 and 10 are the products of the reaction at 48 hr of asialo-rFSH and CMP-SA-PEG (10 kDa) at 0.5 mM and 1.0 mM, respectively.

Figure 112 is graph of the pharmacokinetics of rFSH and rFSH-SA-PEG (1KDa and 10 KDa). This graph illustrates the relationship between the time a rFSH compound is in the

10   blood stream of the rat, and the mean concentration of the rFSH compound in the blood for glycoPEGylated rFSH as compared to non-PEGylated rFSH.

Figure 113 is a graph of the results of the FSH bioassay using Sertoli cells. This graph illustrates the relationship between the FSH concentration in the Sertoli cell incubation medium and the amount of 17-β estradiol released from the Sertoli cells.

15   Figure 114 is an image of an SDS-PAGE gel: standard (Lane 1); native transferrin (Lane 2); asialotransferrin (Lane 3); asialotransferrin and CMP-SA (Lane 4); Lanes 5 and 6, asialotransferrin and CMP-SA-PEG (1 kDa) at 0.5 mM and 5 mM, respectively; Lanes 7 and 8, asialotransferrin and CMP-SA-PEG (5 kDa) at 0.5 mM and 5 mM, respectively; Lanes 9 and 10, asialotransferrin and CMP-SA-PEG (10 kDa) at 0.5 mM and 5 mM, respectively.

20   Figure 115 is an image of an IEF gel: native transferrin (Lane 1); asialotransferrin (Lane 2); asialotransferrin and CMP-SA, 24hr (Lane 3); asialotransferrin and CMP-SA, 96 hr (Lane 4) Lanes 5 and 6, asialotransferrin and CMP-SA-PEG (1 kDa) at 24 hr and 96 hr, respectively; Lanes 7 and 8, asialotransferrin and CMP-SA-PEG (5 kDa) at 24 hr and 96 hr, respectively; Lanes 9 and 10, asialotransferrin and CMP-SA-PEG (10 kDa) at 24 hr and 96

25   hr, respectively.

Figure 116 is an image of an isoelectric focusing gel (pH 3-7) of asialo-Factor VIIa. Lane 1 is rFactor VIIa; lanes 2-5 are asialo-Factor VIIa.

Figure 117 is a graph of a MALDI spectra of Factor VIIa.

Figure 118 is a graph of a MALDI spectra of Factor VIIa-PEG (1 kDa).

30   Figure 119 is a graph depicting a MALDI spectra of Factor VIIa-PEG (10 kDa).

Figure 120 is an image of an SDS-PAGE gel of PEGylated Factor VIIa. Lane 1 is asialo-Factor VIIa. Lane 2 is the product of the reaction of asialo-Factor VIIa and CMP-SA-PEG(1 kDa) with ST3Gal3 after 48 hr. Lane 3 is the product of the reaction of asialo-Factor VIIa and CMP-SA-PEG (1 kDa) with ST3Gal3 after 48 hr. Lane 4 is the product of the

5   reaction of asialo-Factor VIIa and CMP-SA-PEG (10 kDa) with ST3Gal3 at 96 hr.

Figure 121 is an image of an IEF gel depicting the pI of the products of the desialylation procedure. Lanes 1 and 5 are IEF standards. Lane 2 is Factor IX protein. Lane 3 is rFactor IX protein. Lane 4 is the desialylation reaction of rFactor IX protein at 20 hr.

Figure 122 is an image of an SDS-PAGE gel depicting the molecular weight of Factor

10   IX conjugated with either SA-PEG (1 kDa) or SA-PEG (10 kDa) after reaction with CMP-SA-PEG. Lanes 1 and 6 are SeeBlue +2 molecular weight standards. Lane 2 is rF-IX. Lane 3 is desialylated rF-IX. Lane 4 is rFactor IX conjugated to SA-PEG (1 kDa). Lane 5 is rFactor IX conjugated to SA-PEG (10 kDa).

Figure 123 is an image of an SDS-PAGE gel depicting the reaction products of direct-

15   sialylation of Factor-IX and sialic acid capping of Factor-IX-SA-PEG. Lane 1 is protein standards, lane 2 is blank; lane 3 is rFactor-IX; lane 4 is SA capped rFactor-IX-SA-PEG (10 KDa); lane 5 is rFactor-IX-SA-PEG (10 KDa); lane 6 is ST3Gal1; lane 7 is ST3Gal3; lanes 8, 9, 10 are rFactor-IX-SA-PEG(10 KDa) with no prior sialidase treatment.

Figure 124 is a graph depicting a MALDI spectrum the glycans of native EPO.

20   Figure 125 is an image of an SDS-PAGE gel of the products of the PEGylation reactions using CMP-NAN-PEG (1KDa), and CMP-NAN-PEG (10KDa).

Figure 126 is a graph depicting the results of the *in vitro* bioassay of PEGylated EPO. Diamonds represent the data from sialylated EPO having no PEG molecules. Squares represent the data obtained using EPO with PEG (1KDa). Triangles represent the data

25   obtained using EPO with PEG (10KDa).

DETAILED DESCRIPTION OF THE INVENTION

The present invention includes methods and compositions for the cell free *in vitro* addition and/or deletion of sugars to or from a peptide molecule in such a manner as to

30   provide a glycopeptide molecule having a specific customized or desired glycosylation

pattern, wherein the glycopeptide is produced at an industrial scale. In a preferred embodiment of the invention, the glycopeptide so produced has attached thereto a modified sugar that has been added to the peptide via an enzymatic reaction. A key feature of the invention is to take a peptide produced by any cell type and generate a core glycan structure

5   on the peptide, following which the glycan structure is then remodeled *in vitro* to generate a glycopeptide having a glycosylation pattern suitable for therapeutic use in a mammal. More specifically, it is possible according to the present invention, to prepare a glycopeptide molecule having a modified sugar molecule or other compound conjugated thereto, such that the conjugated molecule confers a beneficial property on the peptide. According to the

10   present invention, the conjugate molecule is added to the peptide enzymatically because enzyme-based addition of conjugate molecules to peptides has the advantage of regioselectivity and stereoselectivity. It is therefore possible, using the methods and compositions provided herein, to remodel a peptide to confer upon the peptide a desired glycan structure preferably having a modified sugar attached thereto. It is also possible,

15   using the methods and compositions of the invention to generate peptide molecules having desired and or modified glycan structures at an industrial scale, thereby, for the first time, providing the art with a practical solution for the efficient production of improved therapeutic peptides.

Definitions

20   Unless defined otherwise, all technical and scientific terms used herein generally have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. Generally, the nomenclature used herein and the laboratory procedures in cell culture, molecular genetics, organic chemistry, and nucleic acid chemistry and hybridization are those well known and commonly employed in the art. Standard techniques

25   are used for nucleic acid and peptide synthesis. The techniques and procedures are generally performed according to conventional methods in the art and various general references (e.g., Sambrook et al., 1989, Molecular Cloning: A Laboratory Manual, 2d ed. Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY), which are provided throughout this document. The nomenclature used herein and the laboratory procedures used in analytical chemistry and

30   organic syntheses described below are those well known and commonly employed in the art.

Standard techniques or modifications thereof, are used for chemical syntheses and chemical analyses.

The articles "a" and "an" are used herein to refer to one or to more than one (i.e. to at least one) of the grammatical object of the article. By way of example, "an element" means

5 one element or more than one element.

The term "antibody," as used herein, refers to an immunoglobulin molecule which is able to specifically bind to a specific epitope on an antigen. Antibodies can be intact immunoglobulins derived from natural sources or from recombinant sources and can be immunoreactive portions of intact immunoglobulins. Antibodies are typically tetramers of

10 immunoglobulin molecules. The antibodies in the present invention may exist in a variety of forms including, for example, polyclonal antibodies, monoclonal antibodies, Fv, Fab and F(ab)₂, as well as single chain antibodies and humanized antibodies (Harlow et al., 1999, Using Antibodies: A Laboratory Manual, Cold Spring Harbor Laboratory Press, NY; Harlow et al., 1989, Antibodies: A Laboratory Manual, Cold Spring Harbor, New York; Houston et

15 al., 1988, Proc. Natl. Acad. Sci. USA 85:5879-5883; Bird et al., 1988, Science 242:423-426).

By the term "synthetic antibody" as used herein, is meant an antibody which is generated using recombinant DNA technology, such as, for example, an antibody expressed by a bacteriophage as described herein. The term should also be construed to mean an antibody which has been generated by the synthesis of a DNA molecule encoding the

20 antibody and which DNA molecule expresses an antibody protein, or an amino acid sequence specifying the antibody, wherein the DNA or amino acid sequence has been obtained using synthetic DNA or amino acid sequence technology which is available and well known in the art.

As used herein, a "functional" biological molecule is a biological molecule in a form

25 in which it exhibits a property by which it is characterized. A functional enzyme, for example, is one which exhibits the characteristic catalytic activity by which the enzyme is characterized.

As used herein, the structure " ξ——AA " , is the point of connection between an amino acid in the peptide chain and the glycan structure.

30 "N-linked" oligosaccharides are those oligosaccharides that are linked to a peptide backbone through asparagine, by way of an asparagine-N-acetylglucosamine linkage. N-

linked oligosaccharides are also called "N-glycans." All N-linked oligosaccharides have a common pentasaccharide core of $Man_3GlcNAc_2$. They differ in the presence of, and in the number of branches (also called antennae) of peripheral sugars such as N-acetylglucosamine, galactose, N-acetylgalactosamine, fucose and sialic acid. Optionally, this structure may also

5   contain a core fucose molecule and/or a xylose molecule.

An "elemental trimannosyl core structure" refers to a glycan moiety comprising solely a trimannosyl core structure, with no additional sugars attached thereto. When the term "elemental" is not included in the description of the "trimannosyl core structure," then the glycan comprises the trimannosyl core structure with additional sugars attached thereto.

10   Optionally, this structure may also contain a core fucose molecule and/or a xylose molecule.

The term "elemental trimannosyl core glycopeptide" is used herein to refer to a glycopeptide having glycan structures comprised primarily of an elemental trimannosyl core structure. Optionally, this structure may also contain a core fucose molecule and/or a xylose molecule.

15   "O-linked" oligosaccharides are those oligosaccharides that are linked to a peptide backbone through threonine or serine.

All oligosaccharides described herein are described with the name or abbreviation for the non-reducing saccharide (i.e., Gal), followed by the configuration of the glycosidic bond (α or β), the ring bond (1 or 2), the ring position of the reducing saccharide involved in the

20   bond (2, 3, 4, 6 or 8), and then the name or abbreviation of the reducing saccharide (i.e., GlcNAc). Each saccharide is preferably a pyranose. For a review of standard glycobiology nomenclature see, Essentials of Glycobiology Varki et al. eds., 1999, CSHL Press.

The term "sialic acid" refers to any member of a family of nine-carbon carboxylated sugars. The most common member of the sialic acid family is N-acetyl-neuraminic acid (2-

25   keto-5-acetamido-3,5-dideoxy-D-glycero-D-galactononulopyranos-1-onic acid (often abbreviated as Neu5Ac, NeuAc, or NANA). A second member of the family is N-glycolyl-neuraminic acid (Neu5Gc or NeuGc), in which the N-acetyl group of NeuAc is hydroxylated. A third sialic acid family member is 2-keto-3-deoxy-nonulosonic acid (KDN) (Nadano *et al.* (1986) *J. Biol. Chem.* **261**: 11550-11557; Kanamori *et al.*, *J. Biol. Chem.* **265**: 21811-21819

30   (1990)). Also included are 9-substituted sialic acids such as a 9-O-C_1-C_6 acyl-Neu5Ac like 9-O-lactyl-Neu5Ac or 9-O-acetyl-Neu5Ac, 9-deoxy-9-fluoro-Neu5Ac and 9-azido-9-deoxy-

NeuSAc. For review of the sialic acid family, *see, e.g.,* Varki, *Glycobiology* 2: 25-40 (1992); *Sialic Acids: Chemistry, Metabolism and Function,* R. Schauer, Ed. (Springer-Verlag, New York (1992)). The synthesis and use of sialic acid compounds in a sialylation procedure is disclosed in international application WO 92/16640, published October 1, 1992.

5   A peptide having "desired glycosylation", as used herein, is a peptide that comprises one or more oligosaccharide molecules which are required for efficient biological activity of the peptide.

A "disease" is a state of health of an animal wherein the animal cannot maintain homeostasis, and wherein if the disease is not ameliorated then the animal's health continues

10   to deteriorate.

The "area under the curve" or "AUC", as used herein in the context of administering a peptide drug to a patient, is defined as total area under the curve that describes the concentration of drug in systemic circulation in the patient as a function of time from zero to infinity.

15   The term "half-life" or "t ½", as used herein in the context of administering a peptide drug to a patient, is defined as the time required for plasma concentration of a drug in a patient to be reduced by one half. There may be more than one half-life associated with the peptide drug depending on multiple clearance mechanisms, redistribution, and other mechanisms well known in the art. Usually, alpha and beta half-lives are defined such that

20   the alpha phase is associated with redistribution, and the beta phase is associated with clearance. However, with protein drugs that are, for the most part, confined to the bloodstream, there can be at least two clearance half-lives. For some glycosylated peptides, rapid beta phase clearance may be mediated via receptors on macrophages, or endothelial cells that recognize terminal galactose, N-acetylgalactosamine, N-acetylglucosamine,

25   mannose, or fucose. Slower beta phase clearance may occur via renal glomerular filtration for molecules with an effective radius < 2 nm (approximately 68 kD) and/or specific or non-specific uptake and metabolism in tissues. GlycoPEGylation may cap terminal sugars (e.g. galactose or N-acetylgalactosamine) and thereby block rapid alpha phase clearance via receptors that recognize these sugars. It may also confer a larger effective radius and thereby

30   decrease the volume of distribution and tissue uptake, thereby prolonging the late beta phase. Thus, the precise impact of glycoPEGylation on alpha phase and beta phase half-lives will

vary depending upon the size, state of glycosylation, and other parameters, as is well known in the art. Further explanation of "half-life" is found in Pharmaceutical Biotechnology (1997, DFA Crommelin and RD Sindelar, eds., Harwood Publishers, Amsterdam, pp 101 – 120).

5   The term "residence time", as used herein in the context of administering a peptide drug to a patient, is defined as the average time that drug stays in the body of the patient after dosing.

An "isolated nucleic acid" refers to a nucleic acid segment or fragment which has been separated from sequences which flank it in a naturally occurring state, e.g., a DNA

10   fragment which has been removed from the sequences which are normally adjacent to the fragment, e.g., the sequences adjacent to the fragment in a genome in which it naturally occurs. The term also applies to nucleic acids which have been substantially purified from other components which naturally accompany the nucleic acid, e.g., RNA or DNA or proteins, which naturally accompany it in the cell. The term therefore includes, for example,

15   a recombinant DNA which is incorporated into a vector, into an autonomously replicating plasmid or virus, or into the genomic DNA of a prokaryote or eukaryote, or which exists as a separate molecule (e.g., as a cDNA or a genomic or cDNA fragment produced by PCR or restriction enzyme digestion) independent of other sequences. It also includes a recombinant DNA which is part of a hybrid nucleic acid encoding additional peptide sequence.

20   A "polynucleotide" means a single strand or parallel and anti-parallel strands of a nucleic acid. Thus, a polynucleotide may be either a single-stranded or a double-stranded nucleic acid.

The term "nucleic acid" typically refers to large polynucleotides. The term "oligonucleotide" typically refers to short polynucleotides, generally no greater than about 50

25   nucleotides.

Conventional notation is used herein to describe polynucleotide sequences: the left-hand end of a single-stranded polynucleotide sequence is the 5'-end; the left-hand direction of a double-stranded polynucleotide sequence is referred to as the 5'-direction. The direction of 5' to 3' addition of nucleotides to nascent RNA transcripts is referred to as the transcription

30   direction. The DNA strand having the same sequence as an mRNA is referred to as the "coding strand"; sequences on the DNA strand which are located 5' to a reference point on the

DNA are referred to as "upstream sequences"; sequences on the DNA strand which are 3' to a reference point on the DNA are referred to as "downstream sequences."

"Encoding" refers to the inherent property of specific sequences of nucleotides in a polynucleotide, such as a gene, a cDNA, or an mRNA, to serve as templates for synthesis of
5   other polymers and macromolecules in biological processes having either a defined sequence of nucleotides (i.e., rRNA, tRNA and mRNA) or a defined sequence of amino acids and the biological properties resulting therefrom. Thus, a nucleic acid sequence encodes a protein if transcription and translation of mRNA corresponding to that nucleic acid produces the protein in a cell or other biological system. Both the coding strand, the nucleotide sequence
10 of which is identical to the mRNA sequence and is usually provided in sequence listings, and the non-coding strand, used as the template for transcription of a gene or cDNA, can be referred to as encoding the protein or other product of that nucleic acid or cDNA.

Unless otherwise specified, a "nucleotide sequence encoding an amino acid sequence" includes all nucleotide sequences that are degenerate versions of each other and that encode
15 the same amino acid sequence. Nucleotide sequences that encode proteins and RNA may include introns.

"Homologous" as used herein, refers to the subunit sequence similarity between two polymeric molecules, e.g., between two nucleic acid molecules, e.g., two DNA molecules or two RNA molecules, or between two peptide molecules. When a subunit position in both of
20 the two molecules is occupied by the same monomeric subunit, e.g., if a position in each of two DNA molecules is occupied by adenine, then they are homologous at that position. The homology between two sequences is a direct function of the number of matching or homologous positions, e.g., if half (e.g., five positions in a polymer ten subunits in length) of the positions in two compound sequences are homologous then the two sequences are 50%
25 homologous, if 90% of the positions, e.g., 9 of 10, are matched or homologous, the two sequences share 90% homology. By way of example, the DNA sequences 3'ATTGCC5' and 3'TATGGC share 50% homology.

As used herein, "homology" is used synonymously with "identity."

The determination of percent identity between two nucleotide or amino acid
30 sequences can be accomplished using a mathematical algorithm. For example, a mathematical algorithm useful for comparing two sequences is the algorithm of Karlin and

Altschul (1990, Proc. Natl. Acad. Sci. USA 87:2264-2268), modified as in Karlin and

Altschul (1993, Proc. Natl. Acad. Sci. USA 90:5873-5877). This algorithm is incorporated

into the NBLAST and XBLAST programs of Altschul, et al. (1990, J. Mol. Biol. 215:403-

410), and can be accessed, for example at the National Center for Biotechnology Information

5   (NCBI) world wide web site having the universal resource locator

"http://www.ncbi.nlm.nih.gov/BLAST/". BLAST nucleotide searches can be performed with

the NBLAST program (designated "blastn" at the NCBI web site), using the following

parameters: gap penalty = 5; gap extension penalty = 2; mismatch penalty = 3; match reward

= 1; expectation value 10.0; and word size = 11 to obtain nucleotide sequences homologous

10   to a nucleic acid described herein. BLAST protein searches can be performed with the

XBLAST program (designated "blastn" at the NCBI web site) or the NCBI "blastp" program,

using the following parameters: expectation value 10.0, BLOSUM62 scoring matrix to

obtain amino acid sequences homologous to a protein molecule described herein. To obtain

gapped alignments for comparison purposes, Gapped BLAST can be utilized as described in

15   Altschul et al. (1997, Nucleic Acids Res. 25:3389-3402). Alternatively, PSI-Blast or PHI-

Blast can be used to perform an iterated search which detects distant relationships between

molecules (Id.) and relationships between molecules which share a common pattern. When

utilizing BLAST, Gapped BLAST, PSI-Blast, and PHI-Blast programs, the default

parameters of the respective programs (e.g., XBLAST and NBLAST) can be used. See

20   http://www.ncbi.nlm.nih.gov.

     The percent identity between two sequences can be determined using techniques

similar to those described above, with or without allowing gaps. In calculating percent

identity, typically exact matches are counted.

     A "heterologous nucleic acid expression unit" encoding a peptide is defined as a

25   nucleic acid having a coding sequence for a peptide of interest operably linked to one or

more expression control sequences such as promoters and/or repressor sequences wherein at

least one of the sequences is heterologous, i. e., not normally found in the host cell.

     By describing two polynucleotides as "operably linked" is meant that a single-

stranded or double-stranded nucleic acid moiety comprises the two polynucleotides arranged

30   within the nucleic acid moiety in such a manner that at least one of the two polynucleotides is

able to exert a physiological effect by which it is characterized upon the other. By way of

example, a promoter operably linked to the coding region of a nucleic acid is able to promote transcription of the coding region.

As used herein, the term "promoter/regulatory sequence" means a nucleic acid sequence which is required for expression of a gene product operably linked to the
5   promoter/regulator sequence. In some instances, this sequence may be the core promoter sequence and in other instances, this sequence may also include an enhancer sequence and other regulatory elements which are required for expression of the gene product. The promoter/regulatory sequence may, for example, be one which expresses the gene product in a tissue specific manner.
10   A "constitutive promoter is a promoter which drives expression of a gene to which it is operably linked, in a constant manner in a cell. By way of example, promoters which drive expression of cellular housekeeping genes are considered to be constitutive promoters.

An "inducible" promoter is a nucleotide sequence which, when operably linked with a polynucleotide which encodes or specifies a gene product, causes the gene product to be
15   produced in a living cell substantially only when an inducer which corresponds to the promoter is present in the cell.

A "tissue-specific" promoter is a nucleotide sequence which, when operably linked with a polynucleotide which encodes or specifies a gene product, causes the gene product to be produced in a living cell substantially only if the cell is a cell of the tissue type
20   corresponding to the promoter.

A "vector" is a composition of matter which comprises an isolated nucleic acid and which can be used to deliver the isolated nucleic acid to the interior of a cell. Numerous vectors are known in the art including, but not limited to, linear polynucleotides, polynucleotides associated with ionic or amphiphilic compounds, plasmids, and viruses.
25   Thus, the term "vector" includes an autonomously replicating plasmid or a virus. The term should also be construed to include non-plasmid and non-viral compounds which facilitate transfer of nucleic acid into cells, such as, for example, polylysine compounds, liposomes, and the like. Examples of viral vectors include, but are not limited to, adenoviral vectors, adeno-associated virus vectors, retroviral vectors, and the like.
30   "Expression vector" refers to a vector comprising a recombinant polynucleotide comprising expression control sequences operatively linked to a nucleotide sequence to be

expressed. An expression vector comprises sufficient cis-acting elements for expression; other elements for expression can be supplied by the host cell or in an *in vitro* expression system. Expression vectors include all those known in the art, such as cosmids, plasmids (e.g., naked or contained in liposomes) and viruses that incorporate the recombinant

5   polynucleotide.

A "genetically engineered" or "recombinant" cell is a cell having one or more modifications to the genetic material of the cell. Such modifications are seen to include, but are not limited to, insertions of genetic material, deletions of genetic material and insertion of genetic material that is extrachromasomal whether such material is stably maintained or not.

10   A "peptide" is an oligopeptide, polypeptide, peptide, protein or glycoprotein. The use of the term "peptide" herein includes a peptide having a sugar molecule attached thereto when a sugar molecule is attached thereto.

As used herein, "native form" means the form of the peptide when produced by the cells and/or organisms in which it is found in nature. When the peptide is produced by a

15   plurality of cells and/or organisms, the peptide may have a variety of native forms.

"Peptide" refers to a polymer in which the monomers are amino acids and are joined together through amide bonds, alternatively referred to as a peptide. Additionally, unnatural amino acids, for example, β-alanine, phenylglycine and homoarginine are also included. Amino acids that are not nucleic acid-encoded may also be used in the present invention.

20   Furthermore, amino acids that have been modified to include reactive groups, glycosylation sites, polymers, therapeutic moieties, biomolecules and the like may also be used in the invention. All of the amino acids used in the present invention may be either the D - or L – isomer thereof. The L -isomer is generally preferred. In addition, other peptidomimetics are also useful in the present invention. As used herein, "peptide" refers to both glycosylated and

25   unglycosylated peptides. Also included are peptides that are incompletely glycosylated by a system that expresses the peptide. For a general review, *see*, Spatola, A. F., in CHEMISTRY AND BIOCHEMISTRY OF AMINO ACIDS, PEPTIDES AND PROTEINS, B. Weinstein, eds., Marcel Dekker, New York, p. 267 (1983).

The term "peptide conjugate," refers to species of the invention in which a peptide is

30   conjugated with a modified sugar as set forth herein.

The term "amino acid" refers to naturally occurring and synthetic amino acids, as well as amino acid analogs and amino acid mimetics that function in a manner similar to the naturally occurring amino acids. Naturally occurring amino acids are those encoded by the genetic code, as well as those amino acids that are later modified, *e.g.*, hydroxyproline, γ-

5 carboxyglutamate, and O-phosphoserine. Amino acid analogs refers to compounds that have the same basic chemical structure as a naturally occurring amino acid, *i.e.*, an α carbon that is bound to a hydrogen, a carboxyl group, an amino group, and an R group, *e.g.*, homoserine, norleucine, methionine sulfoxide, methionine methyl sulfonium. Such analogs have modified R groups (*e.g.*, norleucine) or modified peptide backbones, but retain the same basic chemical

10 structure as a naturally occurring amino acid. Amino acid mimetics refers to chemical compounds that have a structure that is different from the general chemical structure of an amino acid, but that function in a manner similar to a naturally occurring amino acid.

As used herein, amino acids are represented by the full name thereof, by the three letter code corresponding thereto, or by the one-letter code corresponding thereto, as

15 indicated in the following Table 1:

Table 1: Amino acids, and the three letter and one letter codes.

Full Name	Three-Letter Code	One-Letter Code
Aspartic Acid	Asp	D
Glutamic Acid	Glu	E
Lysine	Lys	K
Arginine	Arg	R
Histidine	His	H
Tyrosine	Tyr	Y
Cysteine	Cys	C
Asparagine	Asn	N
Glutamine	Gln	Q
Serine	Ser	S
Threonine	Thr	T
Glycine	Gly	G
Alanine	Ala	A
Valine	Val	V
Leucine	Leu	L
Isoleucine	Ile	I
Methionine	Met	M
Proline	Pro	P
Phenylalanine	Phe	F
Tryptophan	Trp	W

The present invention also provides for analogs of proteins or peptides which comprise a protein as identified above. Analogs may differ from naturally occurring proteins or peptides by conservative amino acid sequence differences or by modifications which do not affect sequence, or by both. For example, conservative amino acid changes may be

5   made, which although they alter the primary sequence of the protein or peptide, do not normally alter its function. Conservative amino acid substitutions typically include substitutions within the following groups:

glycine, alanine;

valine, isoleucine, leucine;

10   aspartic acid, glutamic acid;

asparagine, glutamine;

serine, threonine;

lysine, arginine;

phenylalanine, tyrosine.

15

Modifications (which do not normally alter primary sequence) include *in vivo*, or *in vitro*, chemical derivatization of peptides, e.g., acetylation, or carboxylation. Also included are modifications of glycosylation, e.g., those made by modifying the glycosylation patterns of a peptide during its synthesis and processing or in further processing steps; e.g., by

20   exposing the peptide to enzymes which affect glycosylation, e.g., mammalian glycosylating or deglycosylating enzymes. Also embraced are sequences which have phosphorylated amino acid residues, e.g., phosphotyrosine, phosphoserine, or phosphothreonine.

It will be appreciated, of course, that the peptides may incorporate amino acid residues which are modified without affecting activity. For example, the termini may be

25   derivatized to include blocking groups, i.e. chemical substituents suitable to protect and/or stabilize the N- and C-termini from "undesirable degradation", a term meant to encompass any type of enzymatic, chemical or biochemical breakdown of the compound at its termini which is likely to affect the function of the compound, i.e. sequential degradation of the compound at a terminal end thereof.

30   Blocking groups include protecting groups conventionally used in the art of peptide chemistry which will not adversely affect the *in vivo* activities of the peptide. For example,

suitable N-terminal blocking groups can be introduced by alkylation or acylation of the N-terminus. Examples of suitable N-terminal blocking groups include C_1-C_5 branched or unbranched alkyl groups, acyl groups such as formyl and acetyl groups, as well as substituted forms thereof, such as the acetamidomethyl (Acm), Fmoc or Boc groups. Desamino analogs

5   of amino acids are also useful N-terminal blocking groups, and can either be coupled to the N-terminus of the peptide or used in place of the N-terminal reside. Suitable C-terminal blocking groups, in which the carboxyl group of the C-terminus is either incorporated or not, include esters, ketones or amides. Ester or ketone-forming alkyl groups, particularly lower alkyl groups such as methyl, ethyl and propyl, and amide-forming amino groups such as

10   primary amines (-NH_2), and mono- and di-alkylamino groups such as methylamino, ethylamino, dimethylamino, diethylamino, methylethylamino and the like are examples of C-terminal blocking groups. Descarboxylated amino acid analogues such as agmatine are also useful C-terminal blocking groups and can be either coupled to the peptide's C-terminal residue or used in place of it. Further, it will be appreciated that the free amino and carboxyl

15   groups at the termini can be removed altogether from the peptide to yield desamino and descarboxylated forms thereof without affect on peptide activity.

Other modifications can also be incorporated without adversely affecting the activity and these include, but are not limited to, substitution of one or more of the amino acids in the natural L-isomeric form with amino acids in the D-isomeric form. Thus, the peptide may

20   include one or more D-amino acid resides, or may comprise amino acids which are all in the D-form. Retro-inverso forms of peptides in accordance with the present invention are also contemplated, for example, inverted peptides in which all amino acids are substituted with D-amino acid forms.

Acid addition salts of the present invention are also contemplated as functional

25   equivalents. Thus, a peptide in accordance with the present invention treated with an inorganic acid such as hydrochloric, hydrobromic, sulfuric, nitric, phosphoric, and the like, or an organic acid such as an acetic, propionic, glycolic, pyruvic, oxalic, malic, malonic, succinic, maleic, fumaric, tataric, citric, benzoic, cinnamic, mandelic, methanesulfonic, ethanesulfonic, p-toluenesulfonic, salicyclic and the like, to provide a water soluble salt of the

30   peptide is suitable for use in the invention.

Also included are peptides which have been modified using ordinary molecular biological techniques so as to improve their resistance to proteolytic degradation or to optimize solubility properties or to render them more suitable as a therapeutic agent. Analogs of such peptides include those containing residues other than naturally occurring L-amino

5   acids, e.g., D-amino acids or non-naturally occurring synthetic amino acids. The peptides of the invention are not limited to products of any of the specific exemplary processes listed herein.

As used herein, the term "MALDI" is an abbreviation for Matrix Assisted Laser Desorption Ionization. During ionization, SA-PEG (sialic acid-poly(ethylene glycol)) can be

10   partially eliminated from the N-glycan structure of the glycoprotein.

As used herein, the term "glycosyltransferase," refers to any enzyme/protein that has the ability to transfer a donor sugar to an acceptor moiety.

As used herein, the term "modified sugar," refers to a naturally- or non-naturally-occurring carbohydrate that is enzymatically added onto an amino acid or a glycosyl residue

15   of a peptide in a process of the invention. The modified sugar is selected from a number of enzyme substrates including, but not limited to sugar nucleotides (mono-, di-, and tri-phosphates), activated sugars (e.g., glycosyl halides, glycosyl mesylates) and sugars that are neither activated nor nucleotides.

The "modified sugar" is covalently functionalized with a "modifying group." Useful

20   modifying groups include, but are not limited to, water-soluble polymers, therapeutic moieties, diagnostic moieties, biomolecules and the like. The locus of functionalization with the modifying group is selected such that it does not prevent the "modified sugar" from being added enzymatically to a peptide.

The term "water-soluble" refers to moieties that have some detectable degree of

25   solubility in water. Methods to detect and/or quantify water solubility are well known in the art. Exemplary water-soluble polymers include peptides, saccharides, poly(ethers), poly(amines), poly(carboxylic acids) and the like. Peptides can have mixed sequences or be composed of a single amino acid, e.g. poly(lysine). Similarly, saccharides can be of mixed sequence or composed of a single saccharide subunit, e.g., dextran, amylose, chitosan, and

30   poly(sialic acid). An exemplary poly(ether) is poly(ethylene glycol). Poly(ethylene imine) is an exemplary polyamine, and poly(aspartic) acid is a representative poly(carboxylic acid)

The term, "glycosyl linking group," as used herein refers to a glycosyl residue to which an agent (e.g., water-soluble polymer, therapeutic moiety, biomolecule) is covalently attached. In the methods of the invention, the "glycosyl linking group" becomes covalently attached to a glycosylated or unglycosylated peptide, thereby linking the agent to an amino

5   acid and/or glycosyl residue on the peptide. A "glycosyl linking group" is generally derived from a "modified sugar" by the enzymatic attachment of the "modified sugar" to an amino acid and/or glycosyl residue of the peptide. An "intact glycosyl linking group" refers to a linking group that is derived from a glycosyl moiety in which the individual saccharide monomer that links the conjugate is not degraded, e.g., oxidized, e.g., by sodium

10   metaperiodate. "Intact glycosyl linking groups" of the invention may be derived from a naturally occurring oligosaccharide by addition of glycosyl unit(s) or removal of one or more glycosyl unit from a parent saccharide structure.

The terms "targeting moiety" and "targeting agent", as used herein, refer to species that will selectively localize in a particular tissue or region of the body. The localization is

15   mediated by specific recognition of molecular determinants, molecular size of the targeting agent or conjugate, ionic interactions, hydrophobic interactions and the like. Other mechanisms of targeting an agent to a particular tissue or region are known to those of skill in the art.

As used herein, "therapeutic moiety" means any agent useful for therapy including,

20   but not limited to, antibiotics, anti-inflammatory agents, anti-tumor drugs, cytotoxins, and radioactive agents. "Therapeutic moiety" includes prodrugs of bioactive agents, constructs in which more than one therapeutic moiety is bound to a carrier, e.g., multivalent agents. Therapeutic moiety also includes peptides, and constructs that include peptides. Exemplary peptides include those disclosed in Figure 1 and Tables 5 and 6, herein.

25   As used herein, "anti-tumor drug" means any agent useful to combat cancer including, but not limited to, cytotoxins and agents such as antimetabolites, alkylating agents, anthracyclines, antibiotics, antimitotic agents, procarbazine, hydroxyurea, asparaginase, corticosteroids, interferons and radioactive agents. Also encompassed within the scope of the term "anti-tumor drug," are conjugates of peptides with anti-tumor activity, e.g. TNF-α.

30   Conjugates include, but are not limited to those formed between a therapeutic protein and a

glycoprotein of the invention. A representative conjugate is that formed between PSGL-1 and TNF-α.

As used herein, "a cytotoxin or cytotoxic agent" means any agent that is detrimental to cells. Examples include taxol, cytochalasin B, gramicidin D, ethidium bromide, emetine,
5   mitomycin, etoposide, tenoposide, vincristine, vinblastine, colchicin, doxorubicin, daunorubicin, dihydroxy anthracinedione, mitoxantrone, mithramycin, actinomycin D, 1-dehydrotestosterone, glucocorticoids, procaine, tetracaine, lidocaine, propranolol, and puromycin and analogs or homologs thereof. Other toxins include, for example, ricin, CC-1065 and analogues, the duocarmycins. Still other toxins include diphtheria toxin, and snake
10   venom (e.g., cobra venom).

As used herein, "a radioactive agent" includes any radioisotope that is effective in diagnosing or destroying a tumor. Examples include, but are not limited to, indium-111, cobalt-60 and technetium. Additionally, naturally occurring radioactive elements such as uranium, radium, and thorium, which typically represent mixtures of radioisotopes, are
15   suitable examples of a radioactive agent. The metal ions are typically chelated with an organic chelating moiety.

Many useful chelating groups, crown ethers, cryptands and the like are known in the art and can be incorporated into the compounds of the invention (e.g. EDTA, DTPA, DOTA, NTA, HDTA, etc. and their phosphonate analogs such as DTPP, EDTP, HDTP, NTP, etc).
20   See, for example, Pitt et al., "The Design of Chelating Agents for the Treatment of Iron Overload," In, INORGANIC CHEMISTRY IN BIOLOGY AND MEDICINE; Martell, Ed.; American Chemical Society, Washington, D.C., 1980, pp. 279-312; Lindoy, THE CHEMISTRY OF MACROCYCLIC LIGAND COMPLEXES; Cambridge University Press, Cambridge, 1989; Dugas, BIOORGANIC CHEMISTRY; Springer-Verlag, New York, 1989, and references contained
25   therein.

Additionally, a manifold of routes allowing the attachment of chelating agents, crown ethers and cyclodextrins to other molecules is available to those of skill in the art. See, for example, Meares et al., "Properties of In Vivo Chelate-Tagged Proteins and Polypeptides." In, MODIFICATION OF PROTEINS: FOOD, NUTRITIONAL, AND PHARMACOLOGICAL ASPECTS;"
30   Feeney, et al., Eds., American Chemical Society, Washington, D.C., 1982, pp. 370-387;

Kasina *et al., Bioconjugate Chem.,* **9**: 108-117 (1998); Song *et al., Bioconjugate Chem.,* **8**: 249-255 (1997).

As used herein, "pharmaceutically acceptable carrier" includes any material, which when combined with the conjugate retains the activity of the conjugate activity and is non-
5   reactive with the subject's immune system. Examples include, but are not limited to, any of the standard pharmaceutical carriers such as a phosphate buffered saline solution, water, emulsions such as oil/water emulsion, and various types of wetting agents. Other carriers may also include sterile solutions, tablets including coated tablets and capsules. Typically such carriers contain excipients such as starch, milk, sugar, certain types of clay, gelatin,
10   stearic acid or salts thereof, magnesium or calcium stearate, talc, vegetable fats or oils, gums, glycols, or other known excipients. Such carriers may also include flavor and color additives or other ingredients. Compositions comprising such carriers are formulated by well known conventional methods.

As used herein, "administering" means oral administration, administration as a
15   suppository, topical contact, intravenous, intraperitoneal, intramuscular, intralesional, intranasal or subcutaneous administration, intrathecal administration, or the implantation of a slow-release device *e.g.,* a mini-osmotic pump, to the subject.

The term "isolated" refers to a material that is substantially or essentially free from components, which are used to produce the material. For peptide conjugates of the invention,
20   the term "isolated" refers to material that is substantially or essentially free from components, which normally accompany the material in the mixture used to prepare the peptide conjugate. "Isolated" and "pure" are used interchangeably. Typically, isolated peptide conjugates of the invention have a level of purity preferably expressed as a range. The lower end of the range of purity for the peptide conjugates is about 60%, about 70% or about 80% and the upper end
25   of the range of purity is about 70%, about 80%, about 90% or more than about 90%.

When the peptide conjugates are more than about 90% pure, their purities are also preferably expressed as a range. The lower end of the range of purity is about 90%, about 92%, about 94%, about 96% or about 98%. The upper end of the range of purity is about 92%, about 94%, about 96%, about 98% or about 100% purity.
30   Purity is determined by any art-recognized method of analysis (*e.g.,* band intensity on a silver stained gel, polyacrylamide gel electrophoresis, HPLC, or a similar means).

"Essentially each member of the population," as used herein, describes a characteristic of a population of peptide conjugates of the invention in which a selected percentage of the modified sugars added to a peptide are added to multiple, identical acceptor sites on the peptide. "Essentially each member of the population" speaks to the

5   "homogeneity" of the sites on the peptide conjugated to a modified sugar and refers to conjugates of the invention, which are at least about 80%, preferably at least about 90% and more preferably at least about 95% homogenous.

"Homogeneity," refers to the structural consistency across a population of acceptor moieties to which the modified sugars are conjugated. Thus, in a peptide conjugate of the

10   invention in which each modified sugar moiety is conjugated to an acceptor site having the same structure as the acceptor site to which every other modified sugar is conjugated, the peptide conjugate is said to be about 100% homogeneous. Homogeneity is typically expressed as a range. The lower end of the range of homogeneity for the peptide conjugates is about 60%, about 70% or about 80% and the upper end of the range of purity is about 70%,

15   about 80%, about 90% or more than about 90%.

When the peptide conjugates are more than or equal to about 90% homogeneous, their homogeneity is also preferably expressed as a range. The lower end of the range of homogeneity is about 90%, about 92%, about 94%, about 96% or about 98%. The upper end of the range of purity is about 92%, about 94%, about 96%, about 98% or about 100%

20   homogeneity. The purity of the peptide conjugates is typically determined by one or more methods known to those of skill in the art, e.g., liquid chromatography-mass spectrometry (LC-MS), matrix assisted laser desorption mass time of flight spectrometry (MALDI-TOF), capillary electrophoresis, and the like.

"Substantially uniform glycoform" or a "substantially uniform glycosylation pattern,"

25   when referring to a glycopeptide species, refers to the percentage of acceptor moieties that are glycosylated by the glycosyltransferase of interest (e.g., fucosyltransferase). For example, in the case of a $\alpha 1,2$ fucosyltransferase, a substantially uniform fucosylation pattern exists if substantially all (as defined below) of the Galβ1,4-GlcNAc-R and sialylated analogues thereof are fucosylated in a peptide conjugate of the invention. It will be

30   understood by one of skill in the art, that the starting material may contain glycosylated acceptor moieties (e.g., fucosylated Galβ1,4-GlcNAc-R moieties). Thus, the calculated

percent glycosylation will include acceptor moieties that are glycosylated by the methods of the invention, as well as those acceptor moieties already glycosylated in the starting material.

The term "substantially" in the above definitions of "substantially uniform" generally means at least about 40%, at least about 70%, at least about 80%, or more preferably at least

5　　about 90%, and still more preferably at least about 95% of the acceptor moieties for a particular glycosyltransferase are glycosylated.

Description of the Invention

10　　　　　I. Method to Remodel Glycan Chains

The present invention includes methods and compositions for the *in vitro* addition and/or deletion of sugars to or from a glycopeptide molecule in such a manner as to provide a peptide molecule having a specific customized or desired glycosylation pattern, preferably including the addition of a modified sugar thereto. A key feature of the invention therefore is

15　　to take a peptide produced by any cell type and generate a core glycan structure on the peptide, following which the glycan structure is then remodeled *in vitro* to generate a peptide having a glycosylation pattern suitable for therapeutic use in a mammal.

The importance of the glycosylation pattern of a peptide is well known in the art as are the limitations of present *in vivo* methods for the production of properly glycosylated

20　　peptides, particularly when these peptides are produced using recombinant DNA methodology. Moreover, until the present invention, it has not been possible to generate glycopeptides having a desired glycan structure thereon, wherein the peptide can be produced at industrial scale.

In the present invention, a peptide produced by a cell is enzymatically treated *in vitro*

25　　by the systematic addition of the appropriate enzymes and substrates therefor, such that sugar moieties that should not be present on the peptide are removed, and sugar moieties, optionally including modified sugars, that should be added to the peptide are added in a manner to provide a glycopeptide having "desired glycosylation", as defined elsewhere herein.

A. Method to remodel N-linked glycans

30　　　　　In one aspect, the present invention takes advantage of the fact that most peptides of commercial or pharmaceutical interest comprise a common five sugar structure referred to

herein as the trimannosyl core, which is N-linked to asparagine at the sequence Asn-X-
Ser/Thr on a peptide chain. The elemental trimannosyl core consists essentially of two N-
acetylglucosamine (GlcNAc) residues and three mannose (Man) residues attached to a
peptide, i.e., it comprises these five sugar residues and no additional sugars, except that it

5   may optionally include a fucose residue. The first GlcNAc is attached to the amide group of
the asparagine and the second GlcNAc is attached to the first via a β1,4 linkage. A mannose
residue is attached to the second GlcNAc via a β1,4 linkage and two mannose residues are
attached to this mannose via an α1,3 and an α1,6 linkage respectively. A schematic depiction
of a trimannosyl core structure is shown in Figure 2, left side. While it is the case that glycan

10   structures on most peptides comprise other sugars in addition to the trimannosyl core, the
trimannosyl core structure represents an essential feature of N-linked glycans on mammalian
peptides.

        The present invention includes the generation of a peptide having a trimannosyl core
structure as a fundamental element of the structure of the glycan molecules contained

15   thereon. Given the variety of cellular systems used to produce peptides, whether the systems
are themselves naturally occurring or whether they involve recombinant DNA methodology,
the present invention provides methods whereby a glycan molecule on a peptide produced in
any cell type can be reduced to an elemental trimannosyl core structure. Once the elemental
trimannosyl core structure has been generated then it is possible using the methods described

20   herein, to generate *in vitro*, a desired glycan structure on the peptide which confers on the
peptide one or more properties that enhances the therapeutic effectiveness of the peptide.

        It should be clear from the discussion herein that the term "trimannosyl core" is used
to describe the glycan structure shown in Figure 2, left side. Glycopeptides having a
trimannosyl core structure may also have additional sugars added thereto, and for the most

25   part, do have additional structures added thereto irrespective of whether the sugars give rise
to a peptide having a desired glycan structure. The term "elemental trimannosyl core
structure" is defined elsewhere herein. When the term "elemental" is not included in the
description of the "trimannosyl core structure," then the glycan comprises the trimannosyl
core structure with additional sugars attached thereto.

30   The term "elemental trimannosyl core glycopeptide" is used herein to refer to a
glycopeptide having glycan structures comprised primarily of an elemental trimannosyl core

structure. However, it may also optionally contain a fucose residue attached thereto. As discussed herein, elemental trimannosyl core glycopeptides are one optimal, and therefore preferred, starting material for the glycan remodeling processes of the invention.

Another optimal starting material for the glycan remodeling process of the invention
5   is a glycan structure having a trimannosyl core wherein one or two additional GlcNAc residues are added to each of the α1,3 and the α1,6 mannose residues (see for example, the structure on the second line of Figure 3, second structure in from the left of the figure). This structure is referred to herein as "Man3GlcNAc4." Optionally, this structure may also contain a core fucose molecule. Once the Man3GlcNAc4 structure has been generated then it
10   is possible using the methods described herein, to generate *in vitro*, a desired glycan structure on the glycopeptide which confers on the glycopeptide one or more properties that enhances the therapeutic effectiveness of the peptide.

In their native form, the N-linked glycopeptides of the invention, and particularly the mammalian and human glycopeptides useful in the present invention, are N-linked
15   glycosylated with a trimannosyl core structure and one or more sugars attached thereto.

The terms "glycopeptide" and "glycopolypeptide" are used synonymously herein to refer to peptide chains having sugar moieties attached thereto. No distinction is made herein to differentiate small glycopolypeptides or glycopeptides from large glycopolypeptides or glycopeptides. Thus, hormone molecules having very few amino acids in their peptide chain
20   (e.g., often as few as three amino acids) and other much larger peptides are included in the general terms "glycopolypeptide" and "glycopeptide," provided they have sugar moieties attached thereto. However, the use of the term "peptide" does not preclude that peptide from being a glycopeptide.

An example of an N-linked glycopeptide having desired glycosylation is a peptide
25   having an N-linked glycan having a trimannosyl core with at least one GlcNAc residue attached thereto. This residue is added to the trimannosyl core using N-acetyl glucosaminyltransferase I (GnT-I). If a second GlcNAc residue is added, N-acetyl glucosaminyltransferase II (GnT-II) is used. Optionally, additional GlcNAc residues may be added with GnT-IV and/or GnT-V, and a third bisecting GlcNAc residue may be attached to
30   the β1,4 mannose of the trimannosyl core using N-acetyl glucosaminyltransferase III (GnT-III). Optionally, this structure may be extended by treatment with β1,4 galactosyltransferase

to add a galactose residue to each non-bisecting GlcNAc, and even further optionally, using α2,3 or α2,6-sialyltransferase enzymes, sialic acid residues may be added to each galactose residue. The addition of a bisecting GlcNAc to the glycan is not required for the subsequent addition of galactose and sialic acid residues; however, with respect to the substrate affinity

5   of the rat and human GnT-III enzymes, the presence of one or more of the galactose residues on the glycan precludes the addition of the bisecting GlcNAc in that the galactose-containing glycan is not a substrate for these forms of GnT-III. Thus, in instances where the presence of the bisecting GlcNAc is desired and these forms of GnT-III are used, it is important should the glycan contain added galactose and/or sialic residues, that they are removed prior to the

10   addition of the bisecting GlcNAc. Other forms of GnT-III may not require this specific order of substrates for their activity.

Examples of glycan structures which represent the various aspects of peptides having "desired glycosylation" are shown in the drawings provided herein. The precise procedures for the in vitro generation of a peptide having "desired glycosylation" are described

15   elsewhere herein. However, the invention should in no way be construed to be limited solely to any one glycan structure disclosed herein. Rather, the invention should be construed to include any and all glycan structures which can be made using the methodology provided herein.

In some cases, an elemental trimannosyl core alone may constitute the desired

20   glycosylation of a peptide. For example, a peptide having only a trimannosyl core has been shown to be involved in Gaucher's disease (Mistry et al., 1966, Lancet 348: 1555-1559; Bijsterbosch et al., 1996, Eur. J. Biochem. 237:344-349).

According to the present invention, the following procedures for the generation of peptides having desired glycosylation become apparent.

25   a) Beginning with a glycopeptide having one or more glycan molecules which have as a common feature a trimannosyl core structure and at least one or more of a heterogeneous or homogeneous mixture of one or more sugars added thereto, it is possible to increase the proportion of glycopeptides having an elemental trimannosyl core structure as the sole glycan structure or which have Man3GlcNAc4 as the sole glycan structure. This is accomplished in

30   vitro by the systematic addition to the glycopeptide of an appropriate number of enzymes in an appropriate sequence which cleave the heterogeneous or homogeneous mixture of sugars

on the glycan structure until it is reduced to an elemental trimannosyl core or Man3GlcNAc4 structure. Specific examples of how this is accomplished will depend on a variety of factors including in large part the type of cell in which the peptide is produced and therefore the degree of complexity of the glycan structure(s) present on the peptide initially produced by

5   the cell. Examples of how a complex glycan structure can be reduced to an elemental trimannosyl core or a Man3GlcNAc4 structure are presented in Figure 3, described in detail elsewhere herein.

        b) It is possible to generate a peptide having an elemental trimannosyl core structure as the sole glycan structure on the peptide by isolating a naturally occurring cell whose

10   glycosylation machinery produces such a peptide. DNA encoding a peptide of choice is then transfected into the cell wherein the DNA is transcribed, translated and glycosylated such that the peptide of choice has an elemental trimannosyl core structure as the sole glycan structure thereon. For example, a cell lacking a functional GnT-I enzyme will produce several types of glycopeptides. In some instances, these will be glycopeptides having no additional sugars

15   attached to the trimannosyl core. However, in other instances, the peptides produced may have two additional mannose residues attached to the trimannosyl core, resulting in a Man5 glycan. This is also a desired starting material for the remodeling process of the present invention. Specific examples of the generation of such glycan structures are described herein.

20   c) Alternatively, it is possible to genetically engineer a cell to confer upon it a specific glycosylation machinery such that a peptide having an elemental trimannosyl core or Man3GlcNAc4 structure as the sole glycan structure on the peptide is produced. DNA encoding a peptide of choice is then transfected into the cell wherein the DNA is transcribed, translated and glycosylated such that the peptide of choice has an increased number of

25   glycans comprising solely an elemental trimannosyl core structure. For example, certain types of cells that are genetically engineered to lack GnT-I, may produce a glycan having an elemental trimannosyl core structure, or, depending on the cell, may produce a glycan having a trimannosyl core plus two additional mannose residues attached thereto (Man5). When the cell produces a Man5 glycan structure, the cell may be further genetically engineered to

30   express mannosidase 3 which cleaves off the two additional mannose residues to generate the

trimannosyl core. Alternatively, the Man5 glycan may be incubated *in vitro* with mannosidase 3 to have the same effect.

d) It is readily apparent from the discussion in b) and c) that it is not necessary that the cells produce only peptides having elemental trimannosyl core or Man3GlcNAc4 structures attached thereto. Rather, unless the cells described in b) and c) produce peptides having 100% elemental trimannosyl core structures (i.e., having no additional sugars attached thereto) or 100% of Man3GlcNAc4 structures, the cells in fact produce a heterogeneous mixture of peptides having, in combination, elemental trimannosyl core structures, or Man3GlcNAc4 structures, as the sole glycan structure in addition to these structures having additional sugars attached thereto. The proportion of peptides having a trimannosyl core or Man3GlcNAc4 structure having additional sugars attached thereto, as opposed to those having one structure, will vary depending on the cell which produces them. The complexity of the glycans (i.e. which and how many sugars are attached to the trimannosyl core) will also vary depending on the cell which produces them.

e) Once a glycopeptide having an elemental trimannosyl core or a trimannosyl core with one or two GlcNAc residues attached thereto is produced by following a), b) or c) above, according to the present invention, additional sugar molecules are added *in vitro* to the trimannosyl core structure to generate a peptide having desired glycosylation (i.e., a peptide having an *in vitro* customized glycan structure).

f) However, when it is the case that a peptide having an elemental trimannosyl core or Man3GlcNAc4 structure with some but not all of the desired sugars attached thereto is produced, then it is only necessary to add any remaining desired sugars without reducing the glycan structure to the elemental trimannosyl core or Man3GlcNAc4 structure. Therefore, in some cases, a peptide having a glycan structure having a trimannosyl core structure with additional sugars attached thereto, will be a suitable substrate for remodeling.

Isolation of an elemental trimannosyl core glycopeptide

The elemental trimannosyl core or Man3GlcNAc4 glycopeptides of the invention may be isolated and purified, if necessary, using techniques well known in the art of peptide purification. Suitable techniques include chromatographic techniques, isoelectric focusing techniques, ultrafiltration techniques and the like. Using any such techniques, a composition of the invention can be prepared in which the glycopeptides of the invention are isolated from

other peptides and from other components normally found within cell culture media. The degree of purification can be, for example, 90% with respect to other peptides or 95%, or even higher, e.g., 98%. See, e.g., Deutscher et al. (ed., 1990, Guide to Peptide Purification, Harcourt Brace Jovanovich, San Diego).

5   The heterogeneity of N-linked glycans present in the glycopeptides produced by the prior art methodology generally only permits the isolation of a small portion of the target glycopeptides which can be modified to produce desired glycopeptides. In the present methods, large quantities of elemental trimannosyl core glycopeptides and other desired glycopeptides, including Man3GlcNAc4 glycans, can be produced which can then be further

10   modified to generate large quantities of peptides having desired glycosylation.

Specific enrichment of any particular type of glycan bound to a peptide may be accomplished using lectins which have an affinity for the desired glycan. Such techniques are well known in the art of glycobiology.

A key feature of the invention which is described in more detail below, is that once a

15   core glycan structure is generated on any peptide, the glycan structure is then remodeled *in vitro* to generate a peptide having desired glycosylation that has improved therapeutic use in a mammal. The mammal may be any type of suitable mammal, and is preferably a human.

The various scenarios and the precise methods and compositions for generating peptides with desired glycosylation will become evident from the disclosure which follows.

20   The ultimate objective of the production of peptides for therapeutic use in mammals is that the peptides should comprise glycan structures that facilitate rather than negate the therapeutic benefit of the peptide. As disclosed throughout the present specification, peptides produced in cells may be treated *in vitro* with a variety of enzymes which catalyze the cleavage of sugars that should not be present on the glycan and the addition of sugars which

25   should be present on the glycan such that a peptide having desired glycosylation and thus suitable for therapeutic use in mammals is generated. The generation of different glycoforms of peptides in cells is described above. A variety of mechanisms for the generation of peptides having desired glycosylation is now described, where the starting material i.e., the peptide produced by a cell may differ from one cell type to another. As will become apparent

30   from the present disclosure, it is not necessary that the starting material be uniform with respect to its glycan composition. However, it is preferable that the starting material be

enriched for certain glycoforms in order that large quantities of end product, i.e., correctly glycosylated peptides are produced.

In a preferred embodiment according to the present invention, the degradation and synthesis events that result in a peptide having desired glycosylation involve at some point,

5   the generation of an elemental trimannosyl core structure or a Man3GlcNAc4 structure on the peptide.

The present invention also provides means of adding one or more selected glycosyl residues to a peptide, after which a modified sugar is conjugated to at least one of the selected glycosyl residues of the peptide. The present embodiment is useful, for example, when it is

10   desired to conjugate the modified sugar to a selected glycosyl residue that is either not present on a peptide or is not present in a desired amount. Thus, prior to coupling a modified sugar to a peptide, the selected glycosyl residue is conjugated to the peptide by enzymatic or chemical coupling. In another embodiment, the glycosylation pattern of a peptide is altered prior to the conjugation of the modified sugar by the removal of a carbohydrate residue from

15   the peptide. See for example WO 98/31826.

Addition or removal of any carbohydrate moieties present on the peptide is accomplished either chemically or enzymatically. Chemical deglycosylation is preferably brought about by exposure of the peptide variant to the compound trifluoromethanesulfonic acid, or an equivalent compound. This treatment results in the cleavage of most or all sugars

20   except the linking sugar (N-acetylglucosamine or N-acetylgalactosamine), while leaving the peptide intact. Chemical deglycosylation is described by Hakimuddin et al., 1987, Arch. Biochem. Biophys. 259: 52 and by Edge et al., 1981, Anal. Biochem. 118: 131. Enzymatic cleavage of carbohydrate moieties on peptide variants can be achieved by the use of a variety of endo- and exo-glycosidases as described by Thotakura et al., 1987, Meth. Enzymol. 138:

25   350.

Chemical addition of glycosyl moieties is carried out by any art-recognized method. Enzymatic addition of sugar moieties is preferably achieved using a modification of the methods set forth herein, substituting native glycosyl units for the modified sugars used in the invention. Other methods of adding sugar moieties are disclosed in U.S. Patent No.

30   5,876,980, 6,030,815, 5,728,554, and 5,922,577.

Exemplary attachment points for selected glycosyl residue include, but are not limited to: (a) sites for N- and O-glycosylation; (b) terminal glycosyl moieties that are acceptors for a glycosyltransferase; (c) arginine, asparagine and histidine; (d) free carboxyl groups; (e) free sulfhydryl groups such as those of cysteine; (f) free hydroxyl groups such as those of serine,

5   threonine, or hydroxyproline; (g) aromatic residues such as those of phenylalanine, tyrosine, or tryptophan; or (h) the amide group of glutamine. Exemplary methods of use in the present invention are described in WO 87/05330 published Sep. 11, 1987, and in Aplin and Wriston, CRC Crit. Rev. Biochem., pp. 259-306 (1981).

Dealing specifically with the examples shown in several of the figures provided

10   herein, a description of the sequence of *in vitro* enzymatic reactions for the production of desired glycan structures on peptides is now presented. The precise reaction conditions for each of the enzymatic conversions disclosed below are well known to those skilled in the art of glycobiology and are therefore not repeated here. For a review of the reaction conditions for these types of reactions, see Sadler et al., 1982, Methods in Enzymology 83:458-514 and

15   references cited therein.

In Figure 2 there is shown the structure of an elemental trimannosyl core glycan on the left side. It is possible to convert this structure to a complete glycan structure having a bisecting GlcNAc by incubating the elemental trimannosyl core structure in the presence of GnT-I, followed by GnT-II, and further followed by GnT-III, and a sugar donor comprising

20   UDP-GlcNAc, wherein GlcNAc is sequentially added to the elemental trimannosyl core structure to generate a trimannosyl core having a bisecting GlcNAc.

In Figure 4 there is shown the conversion of a bisecting GlcNAc containing trimannosyl core glycan to a complex glycan structure comprising galactose and N-acetyl neuraminic acid. The bisecting GlcNAc containing trimannosyl core glycan is first incubated

25   with galactosyltransferase and UDP-Gal as a donor molecule, wherein two galactose residues are added to the peripheral GlcNAc residues on the molecule. The enzyme NeuAc-transferase is then used to add two NeuAc residues one to each of the galactose residues.

In Figure 5 there is shown the conversion of a high mannose glycan structure to an elemental trimannosyl core glycan. The high mannose glycan (Man9) is incubated

30   sequentially in the presence of the mannosidase 1 to generate a Man5 structure and then in the presence of mannosidase 3, wherein all but three mannose residues are removed from the

glycan. Alternatively, incubation of the Man9 structure may be trimmed back to the trimannosyl core structure solely by incubation in the presence of mannosidase 3. According to the schemes presented in Figures 2 and 4 above, conversion of this elemental trimannosyl core glycan to a complex glycan molecule is then possible.

5   In Figure 6 there is shown a typical complex N-linked glycan structure produced in plant cells. It is important to note that when plant cells are deficient in GnT-I enzymatic activity, xylose and fucose cannot be added to the glycan. Thus, the use of GnT-I knock-out cells provides a particular advantage in the present invention in that these cells produce peptides having an elemental trimannosyl core onto which additional sugars can be added

10   without performing any "trimming back" reactions. Similarly, in instances where the structure produced in a plant cell may be of the Man5 variety of glycan, if GnT-I is absent in these cells, xylose and fucose cannot be added to the structure. In this case, the Man5 structure may be trimmed back to an elemental trimannosyl core (Man3) using mannosidase 3. According to the methods provided herein, it is now possible to add desired sugar moieties

15   to the trimannosyl core to generate a desired glycan structure.

In Figure 7 there is shown a typical complex N-linked glycan structure produced in insect cells. As is evident, additional sugars, such as, for example, fucose may also be present. Further although not shown here, insect cells may produce high mannose glycans having as many as nine mannose residues and may have additional sugars attached thereto. It

20   is also the case in insect cells that GnT-I knock out cells prevent the addition of fucose residues to the glycan. Thus, production of a peptide in insect cells is preferably accomplished in a GnT-I knock out cell. The glycan thus produced may then be trimmed back *in vitro* if necessary using any of the methods and schemes described herein, and additional sugars may be added *in vitro* thereto also using the methods and schemes provided

25   herein.

In Figure 3 there is shown glycan structures in various stages of completion. Specifically, the *in vitro* enzymatic generation of an elemental trimannosyl core structure from a complex carbohydrate glycan structure which does not contain a bisecting GlcNAc residue is shown. Also shown is the generation of a glycan structure therefrom which

30   contains a bisecting GlcNAc. Several intermediate glycan structures which can be produced are shown. These structures can be produced by cells, or can be produced in the *in vitro*

trimming back reactions described herein. Sugar moieties may be added *in vitro* to the elemental trimannosyl core structure, or to any suitable intermediate structure in order that a desired glycan is produced.

In Figure 8 there is shown a series of possible *in vitro* reactions which can be

5   performed to trim back and add onto glycans beginning with a high mannose structure. For example, a Man9 glycan may be trimmed using mannosidase 1 to generate a Man5 glycan, or it may be trimmed to a trimannosyl core using mannosidase 3 or one or more microbial mannosidases. GnT-I and or GnT-II may then be used to transfer additional GlcNAc residues onto the glycan. Further, there is shown the situation which would not occur when the glycan

10 molecule is produced in a cell that does not have GnT-I (see shaded box). For example, fucose and xylose may be added to a glycan only when GnT-I is active and facilitates the transfer of a GlcNAc to the molecule.

Figure 9 depicts well know strategies for the synthesis of biantennary, triantennary and even tetraantennary glycan structures beginning with the trimannosyl core structure.

15 According to the methods of the invention, it is possible to synthesize each of these structures *in vitro* using the appropriate enzymes and reaction conditions well known in the art of glycobiology.

In Figure 10 there is shown a scheme for the synthesis of yet more complex carbohydrate structures beginning with a trimannosyl core structure. For example, a scheme

20 for the *in vitro* production of Lewis x and Lewis a antigen structures, which may or may not be sialylated is shown. Such structures when present on a peptide may confer on the peptide immunological advantages for upregulating or downregulating the immune response. In addition, such structures are useful for targeting the peptide to specific cells, in that these types of structures are involved in binding to cell adhesion peptides and the like.

25 Figure 11 is an exemplary scheme for preparing an array of O-linked peptides originating with serine or threonine.

Figure 12 is a series of diagrams depicting the four types of O-linked glycan structure termed cores 1 through 4. The core structure is outlined in dotted lines. Sugars which may also be included in this structure include sialic acid residues added to the galactose residues,

30 and fucose residues added to the GlcNAc residues.

Thus, in preferred embodiments, the present invention provides a method of making an N-linked glycosylated glycopeptide by providing an isolated and purified glycopeptide to which is attached an elemental trimannosyl core or a Man3GlcNAc4 structure, contacting the glycopeptide with a glycosyltransferase enzyme and a donor molecule having a glycosyl

5   moiety under conditions suitable to transfer the glycosyl moiety to the glycopeptide. Customization of a trimannosyl core glycopeptide or Man3GlcNAc4 glycopeptide to produce a peptide having a desired glycosylation pattern is then accomplished by the sequential addition of the desired sugar moieties, using techniques well known in the art.

Determination of Glycan Primary Structure

10   When an N-linked glycopeptide is produced by a cell, as noted elsewhere herein, it may comprise a heterogeneous mixture of glycan structures which must be reduced to a common, generally elemental trimannosyl core or Man3GlcNAc4 structure, prior to adding other sugar moieties thereto. In order to determine exactly which sugars should be removed from any particular glycan structure, it is sometimes necessary that the primary glycan

15   structure be identified. Techniques for the determination of glycan primary structure are well know in the art and are described in detail, for example, in Montreuil, "Structure and Biosynthesis of Glycopeptides" In Polysaccharides in Medicinal Applications, pp. 273-327, 1996, Eds. Severian Damitriu, Marcel Dekker, NY. It is therefore a simple matter for one skilled in the art of glycobiology to isolate a population of peptides produced by a cell and

20   determine the structure(s) of the glycans attached thereto. For example, efficient methods are available for (i) the splitting of glycosidic bonds either by chemical cleavage such as hydrolysis, acetolysis, hydrazinolysis, or by nitrous deamination; (ii) complete methylation followed by hydrolysis or methanolysis and by gas-liquid chromatography and mass spectroscopy of the partially methylated monosaccharides; and (iii) the definition of anomeric

25   linkages between monosaccharides using exoglycosidases, which also provide insight into the primary glycan structure by sequential degradation. In particular, the techniques of mass spectroscopy and nuclear magnetic resonance (NMR) spectrometry, especially high field NMR have been successfully used to determine glycan primary structure.
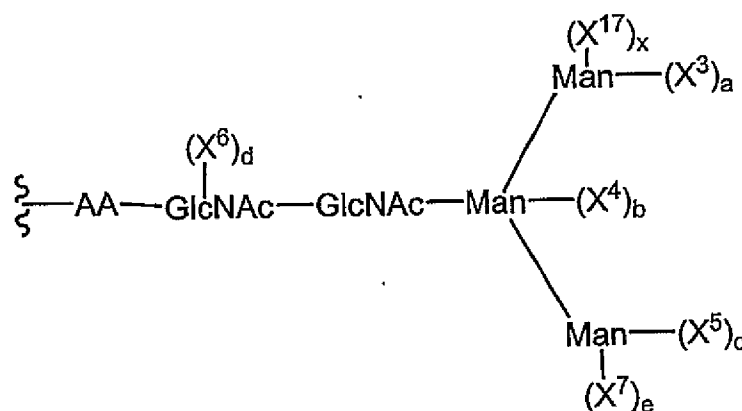
Kits and equipment for carbohydrate analysis are also commercially available.

30   Fluorophore Assisted Carbohydrate Electrophoresis (FACE®) is available from Glyko, Inc. (Novato, CA). In FACE analysis, glycoconjugates are released from the peptide with either

-128-

Endo H or N-glycanase (PNGase F) for N-linked glycans, or hydrazine for Ser/Thr linked glycans. The glycan is then labeled at the reducing end with a fluorophore in a non-structure discriminating manner. The fluorophore labeled glycans are then separated in polyacrylamide gels based on the charge/mass ratio of the saccharide as well as the

5 hydrodynamic volume. Images are taken of the gel under UV light and the composition of the glycans are determined by the migration distance as compared with the standards. Oligosaccharides can be sequenced in this manner by analyzing migration shifts due to the sequential removal of saccharides by exoglycosidase digestion.

Exemplary embodiment

10   The remodeling of N-linked glycosylation is best illustrated with reference to Formula

1:

$$
\begin{array}{c}
\text{(X}^{17}\text{)}_x \\
\mid \\
\text{Man}\text{---(X}^3\text{)}_a \\
/ \\
\text{(X}^6\text{)}_d \\
\mid \qquad\qquad\qquad / \\
\text{\}---AA---GlcNAc---GlcNAc---Man}\text{---(X}^4\text{)}_b \\
\backslash \\
\text{Man}\text{---(X}^5\text{)}_c \\
\mid \\
\text{(X}^7\text{)}_e
\end{array}
$$

where X^3, X^4, X^5, X^6, X^7 and X^{17} are (independently selected) monosaccharide or oligosaccharide residues; and

15   a, b, c, d, e and x are (independently selected) 0, 1 or 2, with the proviso that at least one member selected from a, b, c, d, e and x are 1 or 2.

Formula 1 describes glycan structure comprising the tri-mannosyl core, which is preferably covalently linked to an asparagine residue on a peptide backbone. Preferred

20 expression systems will express and secrete exogenous peptides with N-linked glycans comprising the tri-mannosyl core. Using the remodeling method of the invention, the glycan structures on these peptides can be conveniently remodeled to any glycan structure desired. Exemplary reaction conditions are found throughout the examples and in the literature.

In preferred embodiments, the glycan structures are remodeled so that the structure described in Formula 1 has specific determinates. The structure of the glycan can be chosen to enhance the biological activity of the peptide, give the peptide a new biological activity, remove the biological activity of peptide, or better approximate the glycosylation pattern of the native peptide, among others.

In the first preferred embodiment, the peptide N-linked glycans are remodeled to better approximate the glycosylation pattern of native human proteins. In this embodiment, the glycan structure described in Formula 1 is remodeled to have the following moieties:

X^3 and $X^5 = |$-GlcNAc-Gal-SA;

a and c = 1;

d = 0 or 1;

b, e and x = 0.

This embodiment is particularly advantageous for human peptides expressed in heterologous cellular expression systems. By remodeling the N-linked glycan structures to this configuration, the peptide can be made less immunogenic in a human patient, and/or more stable, among others.

In the second preferred embodiment, the peptide N-linked glycans are remodeled to have a bisecting GlcNAc residue on the tri-mannosyl core. In this embodiment, the glycan structure described in Formula 1 is remodeled to have the following moieties:

X^3 and X^5 are $|$-GlcNAc-Gal-SA;

a and c = 1;

X^4 is GlcNAc;

b=1;

d = 0 or 1;

e and x = 0.

This embodiment is particularly advantageous for recombinant antibody molecules expressed in heterologous cellular systems. When the antibody molecule includes a Fc-mediated cellular cytotoxicity, it is known that the presence of bisected oligosaccharides linked the Fc domain dramatically increased antibody-dependent cellular cytotoxicity.

In a third preferred embodiment, the peptide N-linked glycans are remodeled to have a sialylated Lewis X moiety. In this embodiment, the glycan structure described in Formula 1 is remodeled to have the following moieties:

5

$$X^3 \text{ and } X^5 \text{ are } \overset{\displaystyle Fuc}{\underset{\displaystyle}{\mid}}$$

X^3 and X^5 are ξ——GlcNAc——Gal—SA ;

a, c, d = 1;

b, e and x= 0;

X^6= fucose.
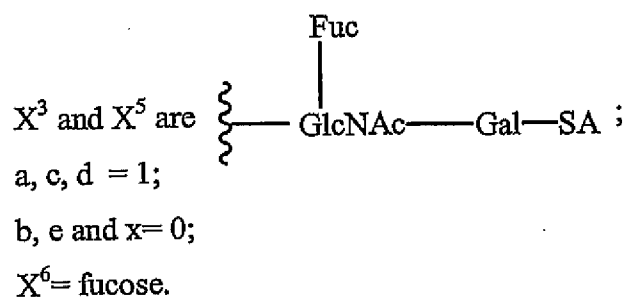
10   This embodiment is particularly advantageous when the peptide which is being remodeling is intended to be targeted to selectin molecules and cells exhibiting the same.

In a fourth preferred embodiment, the peptide N-linked glycans are remodeled to have a conjugated moiety. The conjugated moiety may be a PEG molecule, another peptide, a small molecule such as a drug, among others. In this embodiment, the glycan structure

15   described in Formula 1 is remodeled to have the following moieties:

X^3 and X^5 are |-GlcNAc-Gal-SA-R;

a and c = 1 or 2;

d = 0 or 1;

b, d, e and x = 0;
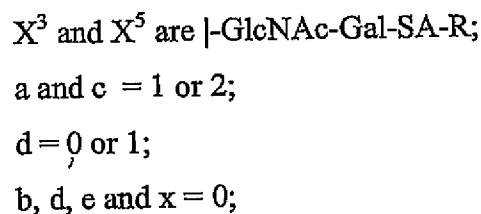
20   where R = conjugate group.

The conjugated moiety may be a PEG molecule, another peptide, a small molecule such as a drug, among others. This embodiment therefore is useful for conjugating the peptide to PEG molecules that will slow the clearance of the peptide from the patient's bloodstream, to peptides that will target both peptides to a specific tissue or cell, or to another peptide of

25   complementary therapeutic use.

It will be clear to one of skill in the art that the invention is not limited to the preferred glycan molecules described above. The preferred embodiments are only a few of the many useful glycan molecules that can be made by the remodeling method of the invention. Those skilled in the art will know how to design other useful glycans.

30   In the first exemplary embodiments, the peptide is expressed in a CHO (Chinese hamster ovarian cell line) according to methods well known in the art. When a peptide with

N-linked glycan consensus sites is expressed and secreted from CHO cells, the N-linked glycans will have the structures depicted in top row of Figure 3. While all of these structures may be present, by far the most common structures are the two at the right side. In the terms of Formula 1,

5   X^3 and X^5 are |-GlcNAc-Gal-(SA);

        a and c = 1;

        b, d, e and x = 0.

Therefore, in one exemplary embodiment, the N-linked glycans of peptides expressed in CHO cells are remodeled to the preferred humanized glycan by contacting the peptides with a

10 glycosyltransferase that is specific for a galactose acceptor molecule and a sialic acid donor molecule. This process is illustrated in Figure 3 and Example 2. In another exemplary embodiment, the N-linked glycans of a peptide expressed and secreted from CHO cells are remodeled to be the preferred PEGylated structures. The peptide is first contacted with a glycosidase specific for sialic acid to remove the terminal SA moiety, and then contacted

15 with a glycosyltransferase specific for a galactose acceptor moiety and an sialic acid acceptor moiety, in the presence of PEG- sialic acid-nucleotide donor molecules. Optionally, the peptide may then be contacted with a glycosyltransferase specific for a galactose acceptor moiety and an sialic acid acceptor moiety, in the presence of sialic acid-nucleotide donor molecules to ensure complete the SA capping of all of the glycan molecules.

20   In other exemplary embodiments, the peptide is expressed in insect cells, such the SF-9 cell line, according to methods well known in the art. When a peptide with N-linked glycan consensus sites is expressed and secreted from SF-9 cells, the N-linked glycans will often have the structures depicted in top row of Figure 7. In the terms of Formula 1:

        X^3 and X^5 are |- GlcNAc;

25   a and c = 0 or 1;

        b = 0;

        X^6 is fucose,

        d = 0, 1 or 2; and

        e and x = 0.

30   The trimannose core is present in the vast majority of the N-linked glycans made by insect cells, and sometimes an antennary GlcNAc and/or fucose residue(s) are also present. In one

exemplary embodiment, the N-linked glycans of a peptide expressed and secreted from insect cells is remodeled to the preferred humanized glycan by first contacting the glycans with a glycosidase specific to fucose molecules, then contacting the glycans with a glycosyltransferases specific to the mannose acceptor molecule on each antennary of the

5   trimannose core, a GlcNAc donor molecule in the presence of nucleotide-GlcNAc molecules; then contacting the glycans with a glycosyltransferase specific to a GlcNAc acceptor molecule, a Gal donor molecule in the presence of nucleotide-Gal molecules; and then contacting the glycans with a glycosyltransferase specific to a galactose acceptor molecule, a sialic acid donor molecule in the presence of nucleotide-SA molecules. One of skill in the art

10   will appreciate that the fucose molecules, if any, can be removed at any time during the procedure. In another exemplary embodiment, the humanized glycan of the previous example is remodeled further to the sialylated Lewis X glycan by contacting the glycan further with a glycosyltransferase specific to a GlcNAc acceptor molecule, a fucose donor molecule in the presence of nucleotide-fucose molecules. This process is illustrated in Figure

15   10 and Example 3.

In yet other exemplary embodiments, the peptide is expressed in yeast, such as *Saccharomyces cerevisiae*, according to methods well known in the art. When a peptide with N-linked glycan consensus sites is expressed and secreted from *S. cerevisiae* cells, the N-linked glycans will have the structures depicted at the left in Figure 5. The N-linked glycans

20   will always have the trimannosyl core, which will often be elaborated with mannose or related polysaccharides of up to 1000 residues. In the terms of Formula 1:

X^3 and X^5 = |-Man -- Man -- $(Man)_{0-1000}$;

a and c =1 or 2;

b, d, e and x = 0.

25   In one exemplary embodiment, the N-linked glycans of a peptide expressed and secreted from yeast cells are remodeled to the elemental trimannose core by first contacting the glycans with a glycosidase specific to $\alpha 2$ mannose molecules, then contacting the glycans with a glycosidase specific to $\alpha 6$ mannose molecules. This process is illustrated in Figure 5 and Example 6. In another exemplary embodiment, the N-linked glycans are further

30   remodeled to make a glycan suitable for an recombinant antibody with Fc-mediated cellular toxicity function by contacting the elemental trimannose core glycans with a

glycosyltransferase specific to the mannose acceptor molecule on each antennary of the trimannose core, a GlcNAc donor molecule in the presence of nucleotide-GlcNAc molecules; then contacting the glycans with a glycosyltransferase specific to the mannose acceptor molecule in the middle of the trimannose core, a GlcNAc donor molecule in the presence of

5   nucleotide-GlcNAc molecules; then contacting the glycans with a glycosyltransferase specific to a GlcNAc acceptor molecule, a Gal donor molecule in the presence of nucleotide-Gal molecules; and then contacting the glycans with a glycosyltransferase specific to a galactose acceptor molecule, a sialic acid donor molecule in the presence of nucleotide-SA molecules. This process is illustrated in Figures 2, 3 and 4.

10   In another exemplary embodiment, the peptide is expressed in bacterial cells, in particular *E. coli* cells, according to methods well known in the art. When a peptide with N-linked glycans consensus sites is expressed in *E. coli* cells, the N-linked consensus sites will not be glycosylated. In an exemplary embodiment, a humanized glycan molecule is built out from the peptide backbone by contacting the peptides with a glycosyltransferase specific for a

15   N-linked consensus site and a GlcNAc donor molecule in the presence of nucleotide-GlcNAc; and further sequentially contacting the growing glycans with glycosyltransferases specific for the acceptor and donor moieties in the present of the required donor moiety until the desired glycan structure is completed. When a peptide with N-linked glycans is expressed in a eukaryotic cells but without the proper leader sequences that direct the nascent

20   peptide to the golgi apparatus, the mature peptide is likely not to be glycosylated. In this case as well the peptide may be given N-linked glycosylation by building out from the peptide N-linked consensus site as aforementioned. When a protein is chemically modified with a sugar moiety, it can be built out as aforementioned.

         These examples are meant to illustrate the invention, and not to limit it. One of skill

25   in the art will appreciate that the steps taken in each example may in some circumstances be able to be performed in a different order to get the same result. One of skill in the art will also understand that a different set of steps may also produce the same resulting glycan. The preferred remodeled glycan is by no means specific to the expression system that the peptide is expressed in. The remodeled glycans are only illustrative and one of skill in the art will

30   know how to take the principles from these examples and apply them to peptides produced in different expression systems to make glycans not specifically described herein.

B. Method to remodel O-linked glycans

O-glycosylation is characterized by the attachment of a variety of monosaccharides in an O-glycosidic linkage to hydroxy amino acids. O-glycosylation is a widespread post-translational modification in the animal and plant kingdoms. The structural complexity of glycans O-linked to proteins vastly exceeds that of N-linked glycans. Serine or threonine residues of a newly translated peptide become modified by virtue of a peptidyl GalNAc transferase in the cis to trans compartments of the Golgi. The site of O-glycosylation is determined not only by the sequence specificity of the glycosyltransferase, but also epigenetic regulation mediated by competition between different substrate sites and competition with other glycosyltransferases responsible for forming the glycan.

The O-linked glycan has been arbitrarily defined as having three regions: the core, the backbone region and the peripheral region. The "core" region of an O-linked glycan is the inner most two or three sugars of the glycan chain proximal to the peptide. The backbone region mainly contributes to the length of the glycan chain formed by uniform elongation. The peripheral region exhibits a high degree of structural complexity. The structural complexity of the O-linked glycans begins with the core structure. In most cases, the first sugar residue added at the O-linked glycan consensus site is GalNAc; however the sugar may also be GlcNAc, glucose, mannose, galactose or fucose, among others. Figure 11 is a diagram of some of the known O-linked glycan core structures and the enzymes responsible for their in vivo synthesis.

In mammalian cells, at least eight different O-linked core structures are found, all based on a core-α-GalNAc residue. The four core structures depicted in Figure 12 are the most common. Core 1 and core 2 are the most abundant structures in mammalian cells, and core 3 and core 4 are found in more restricted, organ-characteristic expression systems. O-linked glycans are reviewed in Montreuil, Structure and Synthesis of Glycopeptides, In Polysaccharides in Medicinal Applications, pp. 273-327, 1996, Eds. Severian Damitriu, Marcel Dekker, NY, and in Schachter and Brockhausen, The Biosynthesis of Branched O-Linked Glycans, 1989, Society for Experimental Biology, pp. 1-26 (Great Britain).

It will be apparent from the present disclosure that the glycan structure of O-glycosylated peptides can be remodeled using similar techniques to those described for N-

linked glycans. O-glycans differ from N-glycans in that they are linked to a serine or threonine residue rather than an asparagine residue. As described herein with respect to N-glycan remodeling, hydrolytic enzymes can be used to cleave unwanted sugar moieties in an O-linked glycan and additional desired sugars can then be added thereto, to build a

5   customized O-glycan structure on the peptide (See Figures 11 and 12).

The initial step in O-glycosylation in mammalian cells is the attachment of N-acetylgalactosamine (GalNAc) using any of a family of at least eleven known α-N-acetylgalactosaminyltransferases, each of which has a restricted acceptor peptide specificity. Generally, the acceptor peptide recognized by each enzyme constitutes a sequence of at least

10   ten amino acids. Peptides that contain the amino acid sequence recognized by one particular GalNAc-transferase become O-glycosylated at the acceptor site if they are expressed in a cell expressing the enzyme and if they are appropriately localized to the Golgi apparatus where UDP-GalNAc is also present.

However, in the case of recombinant proteins, the initial attachment of the GalNAc

15   may not take place. The α-N-acetylgalactosaminyltransferase enzyme native to the expressing cell may have a consensus sequence specificity which differs from that of the recombinant peptide being expressed.

The desired recombinant peptide may be expressed in a bacterial cell, such as *E. coli*, that does not synthesize glycan chains. In these cases, it is advantageous to add the initial

20   GalNAc moiety *in vitro*. The GalNAc moiety can be introduced *in vitro* onto the peptide once the recombinant peptide has been recovered in a soluble form, by contacting the peptide with the appropriate GalNAc transferase in the presence of UDP-GalNAc.

In one embodiment, an additional sequence of amino acids that constitute an effective acceptor for transfer of an O-linked sugar may be present. Such an amino acid sequence is

25   encoded by a DNA sequence fused in frame to the coding sequence of the peptide, or alternatively, may be introduced by chemical means. The peptide may be otherwise lacking glycan chains. Alternately, the peptide may have N- and/or O-linked glycan chains but require an additional glycosylation site, for example, when an additional glycan substituent is desired.

30   In an exemplary embodiment, the amino acid sequence PTTTK-COOH, which is the natural GalNAc acceptor sequence in the human mucin MUC-1, is added as a fusion tag. The

fusion protein is then expressed in *E. coli* and purified. The peptide is then contacted with recombinant human GalNAc-transferases T3 or T6 in the presence of UDP-GalNAc to transfer a GalNAc residue onto the peptide *in vitro*.

This glycan chain on the peptide may then be further elongated using the methods
5   described in reference to the N-linked or O-linked glycans herein. Alternatively, the GalNAc transferase reaction can be carried out in the presence of UDP-GalNAc to which PEG is covalently substituted in the O-3, 4, or 6 positions or the N-2 position. Glycoconjugation is described in detail elswhere herein. Any antigenicity introduced into the peptide by the new peptide sequence can be conveniently masked by PEGylation of the associated glycan. The
10 acceptor site fusion technique can be used to introduce not only a PEG moiety, but to introduce other glycan and non-glycan moieties, including, but not limited to, toxins, anti-infectives, cytotoxic agents, chelators for radionucleotides, and glycans with other functionalities, such as tissue targeting.

15   Exemplary Embodiments
The remodeling of O-linked glycosylation is best illustrated with reference to Formula
2:

$$\begin{array}{c} (X^9)_m \\ | \\ \xi\!-\!AA\!-\!GalNAc\!-\!(Gal)_f\!-\!X^2 \\ | \\ (X^{10})_n \end{array}$$
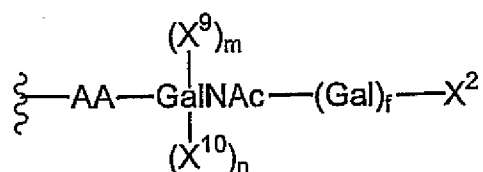
Formula 2 describes a glycan structure comprising a GalNAc which is covalently linked
20 preferably to a serine or threonine residue on a peptide backbone. While this structure is used to illustrate the most common forms of O-linked glycans, it should not be construed to limit the invention solely to these O-linked glycans. Other forms of O-linked glycans are illustrated in Figure 11. Preferred expression systems useful in the present invention express and secrete exogenous peptides having O-linked glycans comprising the GalNAc residue.
25 Using the remodeling methods of the invention, the glycan structures on these peptides can be conveniently remodeled to generate any desired glycan structure. One of skill in the art will appreciate that O-linked glycans can be remodeled using the same principles, enzymes

and reaction conditions as those available in the art once armed with the present disclosure. Exemplary reaction conditions are found throughout the Examples.

In preferred embodiments, the glycan structures are remodeled so that the structure described in Formula 2 has specific moieties. The structure of the glycan may be chosen to

5   enhance the biological activity of the peptide, confer upon the peptide a new biological activity, remove or alter a biological activity of peptide, or better approximate the glycosylation pattern of the native peptide, among others.

In the first preferred embodiment, the peptide O-linked glycans are remodeled to better approximate the glycosylation pattern of native human proteins. In this embodiment,

10   the glycan structure described in Formula 2 is remodeled to have the following moieties:

X^2 is |-SA; or |-SA-SA;

f and n = 0 or 1;

X^{10} is SA;

m = 0.

15   This embodiment is particularly advantageous for human peptides expressed in heterologous cellular expression systems. By remodeling the O-linked glycan structures to have this configuration, the peptide can be rendered less immunogenic in a human patient and/or more stable.

In the another preferred embodiment, the peptide O-linked glycans are remodeled to

20   display a sialylated Lewis X antigen. In this embodiment, the glycan structure described in Formula 2 is remodeled to have the following moieties:

X^2 is |-SA;

X^{10} is Fuc or |-GlcNAc(Fuc)-Gal-SA;

f and n = 1;

25   m = 0.

This embodiment is particularly advantageous when the peptide which is being remodeled is most effective when targeted to a selectin molecule and cells exhibiting the same.

In a yet another preferred embodiment, the peptide O-linked glycans are remodeled to contain a conjugated moiety. The conjugated moiety may be a PEG molecule, another

30   peptide, a small molecule such as a drug, among others. In this embodiment, the glycan structure described in Formula 2 is remodeled to have the following moieties:

X^2 is $|$-SA-R;

$f = 1$;

n and m = 0;

where R is the conjugate group.

5   This embodiment is useful for conjugating the peptide to PEG molecules that will slow the clearance of the peptide from the patient's bloodstream, to peptides that will target both peptides to a specific tissue or cell or to another peptide of complementary therapeutic use.

It will be clear to one of skill in the art that the invention is not limited to the preferred glycan molecules described above. The preferred embodiments are only a few of the many

10   useful glycan molecules that can be made using the remodeling methods of the invention. Those skilled in the art will know how to design other useful glycans once armed with the present invention.

In the first exemplary embodiment, the peptide is expressed in a CHO (Chinese hamster cell line) according to methods well known in the art. When a peptide with O-linked

15   glycan consensus sites is expressed and secreted from CHO cells, the majority of the O-linked glycans will often have the structure, in the terms of Formula 2,

$X^2 = | - SA$;

$f = 1$;

m and n = 0.

20   Therefore, most of the glycans in CHO cells do not require remodeling in order to be acceptable for use in a human patient. In an exemplary embodiment, the O-linked glycans of a peptide expressed and secreted from a CHO cell are remodeled to contain a sialylated Lewis X structure by contacting the glycans with a glycosyltransferase specific for the GalNAc acceptor moiety and the fucose donor moiety in the presence of nucleotide-fucose.

25   This process is illustrated on N-linked glycans in Figure 10 and Example 3.

In other exemplary embodiments, the peptide is expressed in insect cells such as sf9 according to methods well known in the art. When a peptide having O-linked glycan consensus sites is expressed and secreted from most sf9 cells, the majority of the O-linked glycans have the structure, in the terms of Formula 2:

30   $X^2 = H$;

$f = 0$ or 1;

n and m = 0.

See, for example, Marchal et al., (2001, Biol. Chem. 382:151-159). In one exemplary embodiment, the O-linked glycan on a peptide expressed in an insect cell is remodeled to a humanized glycan by contacting the glycans with a glycosyltransferase specific for a GalNAc

5   acceptor molecule and a galactose donor molecule in the presence of nucleotide-Gal; and then contacting the glycans with a glycosyltransferase specific for a Gal acceptor molecule and a SA donor molecule in the presence of nucleotide-SA. In another exemplary embodiment, the O-linked glycans are remodeled further from the humanized form to the sialylated Lewis X form by further contacting the glycans with a glycosyltransferase specific

10 for a GalNAc acceptor molecule and a fucose donor molecule in the presence of nucleotide-fucose.

In yet another exemplary embodiment, the peptide is expressed in fungal cells, in particular *S. cerevisiae* cells, according to methods well known in the art. When a peptide with O-linked glycans consensus sites is expressed and secreted from *S. cerevisiae* cells, the

15 majority of the O-linked glycans have the structure:

| - AA-Man- Man$_{1-2}$.

See Gemmill and Trimble (1999, Biochim. Biophys. Acta 1426:227-237). In order to remodel these O-linked glycans for use in human, it is preferable that the glycan be cleaved at the amino acid level and rebuilt from there.

20 In an exemplary embodiment, the glycan is the O-linked glycan on a peptide expressed in a fungal cell and is remodeled to a humanized glycan by contacting the glycan with an endoglycosylase specific for an amino acid - GalNAc bond; and then contacting the glycan with a glycosyltransferase specific for a O-linked consensus site and a GalNAc donor molecule in the presence of nucleotide-GalNAc; contacting the glycan with a

25 glycosyltransferase specific for a GalNAc acceptor molecule and a galactose donor molecule in the presence of nucleotide-Gal; and then contacting the glycans with a glycosyltransferase specific for a Gal acceptor molecule and a SA donor molecule in the presence of nucleotide-SA.

Alternately, in another exemplary embodiment, the glycan is the O-linked glycan on a

30 peptide expressed in a fungal cell and is remodeled to a humanized glycan by contacting the glycan with an protein O-mannose β-1,2-N-acetylglucosaminyltransferase (POMGnTI) in the

presence of GlcNAc-nucleotide; then contacting the glycan with an galactosyltransferase in the presence of nucleotide-Gal; and then contracting the glycan with an sialyltransferase in the presence of nucleotide-SA.

In another exemplary embodiment, the peptide is expressed in bacterial cells, in

5   particular *E. coli* cells, according to methods well known in the art. When a peptide with an O-linked glycan consensus site is expressed in *E. coli* cells, the O-linked consensus site will not be glycosylated. In this case, the desired glycan molecule must be built out from the peptide backbone in a manner similar to that describe for *S. cerevisiae* expression above. Further, when a peptide having an O-linked glycan is expressed in a eukaryotic cell without

10   the proper leader sequences to direct the nascent peptide to the golgi apparatus, the mature peptide is likely not to be glycosylated. In this case as well, an O-linked glycosyl structure may be added to the peptide by building out the glycan directly from the peptide O-linked consensus site. Further, when a protein is chemically modified with a sugar moiety, it can also be remodeled as described herein.

15   These examples are meant to illustrate the invention, and not to limit it in any way. One of skill in the art will appreciate that the steps taken in each example may in some circumstances be performed in a different order to achieve the same result. One of skill in the art will also understand that a different set of steps may also produce the same resulting glycan. Futher, the preferred remodeled glycan is by no means specific to the expression

20   system that the peptide is expressed in. The remodeled glycans are only illustrative and one of skill in the art will know how to take the principles from these examples and apply them to peptides produced in different expression systems to generate glycans not specifically described herein.

25   C. Glycoconjugation, in general

The invention provides methods of preparing a conjugate of a glycosylated or an unglycosylated peptide. The conjugates of the invention are formed between peptides and diverse species such as water-soluble polymers, therapeutic moieties, diagnostic moieties, targeting moieties and the like. Also provided are conjugates that include two or more

30   peptides linked together through a linker arm, i.e., multifunctional conjugates. The multi-

functional conjugates of the invention can include two or more copies of the same peptide or a collection of diverse peptides with different structures, and/or properties.

       The conjugates of the invention are formed by the enzymatic attachment of a modified sugar to the glycosylated or unglycosylated peptide. The modified sugar, when

5   interposed between the peptide and the modifying group on the sugar becomes what is referred to herein as "an intact glycosyl linking group." Using the exquisite selectivity of enzymes, such as glycosyltransferases, the present method provides peptides that bear a desired group at one or more specific locations. Thus, according to the present invention, a modified sugar is attached directly to a selected locus on the peptide chain or, alternatively,

10   the modified sugar is appended onto a carbohydrate moiety of a peptide. Peptides in which modified sugars are bound to both a peptide carbohydrate and directly to an amino acid residue of the peptide backbone are also within the scope of the present invention.

       In contrast to known chemical and enzymatic peptide elaboration strategies, the methods of the invention make it possible to assemble peptides and glycopeptides that have a

15   substantially homogeneous derivatization pattern; the enzymes used in the invention are generally selective for a particular amino acid residue or combination of amino acid residues of the peptide. The methods are also practical for large-scale production of modified peptides and glycopeptides. Thus, the methods of the invention provide a practical means for large-scale preparation of peptides having preselected substantially uniform derivatization patterns.

20   The methods are particularly well suited for modification of therapeutic peptides, including but not limited to, peptides that are incompletely glycosylated during production in cell culture cells (*e.g.*, mammalian cells, insect cells, plant cells, fungal cells, yeast cells, or prokaryotic cells) or transgenic plants or animals.

       The methods of the invention also provide conjugates of glycosylated and

25   unglycosylated peptides with increased therapeutic half-life due to, for example, reduced clearance rate, or reduced rate of uptake by the immune or reticuloendothelial system (RES). . Moreover, the methods of the invention provide a means for masking antigenic determinants on peptides, thus reducing or eliminating a host immune response against the peptide. Selective attachment of targeting agents can also be used to target a peptide to a particular

30   tissue or cell surface receptor that is specific for the particular targeting agent. Moreover, there is provided a class of peptides that are specifically modified with a therapeutic moiety.

1. The Conjugates

In a first aspect, the present invention provides a conjugate between a peptide and a selected moiety. The link between the peptide and the selected moiety includes an intact glycosyl linking group interposed between the peptide and the selected moiety. As discussed herein, the selected moiety is essentially any species that can be attached to a saccharide unit, resulting in a "modified sugar" that is recognized by an appropriate transferase enzyme, which appends the modified sugar onto the peptide. The saccharide component of the modified sugar, when interposed between the peptide and a selected moiety, becomes an "intact glycosyl linking group." The glycosyl linking group is formed from any mono- or oligo-saccharide that, after modification with a selected moiety, is a substrate for an appropriate transferase.

The conjugates of the invention will typically correspond to the general structure:

$$\left(\left(\text{Peptide}\right)\left(\left(\left(\text{Sugar}\right)_s\text{—}\boxed{\text{Linker}}\text{—}\left(\text{Sugar}\right)_t\text{—}\left(\boxed{\text{Agent}}\right)_a\right)_b\right)_c\right)_d$$
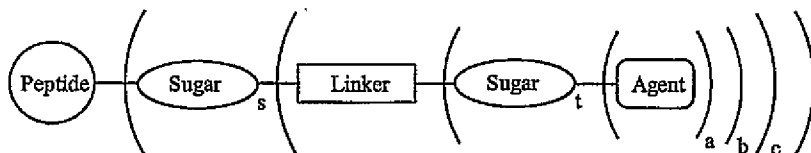
in which the symbols a, b, c, d and s represent a positive, non-zero integer; and t is either 0 or a positive integer. The "agent" is a therapeutic agent, a bioactive agent, a detectable label, water-soluble moiety or the like. The "agent" can be a peptide, e.g., enzyme, antibody, antigen, etc. The linker can be any of a wide array of linking groups, *infra*. Alternatively, the linker may be a single bond or a "zero order linker." The identity of the peptide is without limitation. Exemplary peptides are provided in Figure 1.

In an exemplary embodiment, the selected moiety is a water-soluble polymer. The water-soluble polymer is covalently attached to the peptide via an intact glycosyl linking group. The glycosyl linking group is covalently attached to either an amino acid residue or a glycosyl residue of the peptide. Alternatively, the glycosyl linking group is attached to one or more glycosyl units of a glycopeptide. The invention also provides conjugates in which the glycosyl linking group is attached to both an amino acid residue and a glycosyl residue.

In addition to providing conjugates that are formed through an enzymatically added intact glycosyl linking group, the present invention provides conjugates that are highly homogenous in their substitution patterns. Using the methods of the invention, it is possible

to form peptide conjugates in which essentially all of the modified sugar moieties across a population of conjugates of the invention are attached to multiple copies of a structurally identical amino acid or glycosyl residue. Thus, in a second aspect, the invention provides a peptide conjugate having a population of water-soluble polymer moieties, which are

5   covalently bound to the peptide through an intact glycosyl linking group. In a preferred conjugate of the invention, essentially each member of the population is bound via the glycosyl linking group to a glycosyl residue of the peptide, and each glycosyl residue of the peptide to which the glycosyl linking group is attached has the same structure.

       Also provided is a peptide conjugate having a population of water-soluble polymer

10   moieties covalently bound thereto through an intact glycosyl linking group. In a preferred embodiment, essentially every member of the population of water soluble polymer moieties is bound to an amino acid residue of the peptide via an intact glycosyl linking group, and each amino acid residue having an intact glycosyl linking group attached thereto has the same structure.

15   The present invention also provides conjugates analogous to those described above in which the peptide is conjugated to a therapeutic moiety, diagnostic moiety, targeting moiety, toxin moiety or the like via an intact glycosyl linking group. Each of the above-recited moieties can be a small molecule, natural polymer (e.g., peptide) or synthetic polymer.

       In an exemplary embodiment, interleukin-2 (IL-2) is conjugated to transferrin via a

20   bifunctional linker that includes an intact glycosyl linking group at each terminus of the PEG moiety (Scheme 1). For example, one terminus of the PEG linker is functionalized with an intact sialic acid linker that is attached to transferrin and the other is functionalized with an intact GalNAc linker that is attached to IL-2.

       In another exemplary embodiment, EPO is conjugated to transferrin. In another

25   exemplary embodiment, EPO is conjugated to glial derived neurotropic growth factor (GDNF). In these embodiments, each conjugation is accomplished via a bifunctional linker that includes an intact glycosyl linking group at each terminus of the PEG moiety, as aforementioned. Transferrin transfers the protein across the blood brain barrier.

       As set forth in the Figures appended hereto, the conjugates of the invention can

30   include intact glycosyl linking groups that are mono- or multi-valent (e.g., antennary structures), see, Figures 13-21. The conjugates of the invention also include glycosyl linking

groups that are O-linked glycans originating from serine or threonine (Figure 10). Thus, conjugates of the invention include both species in which a selected moiety is attached to a peptide via a monovalent glycosyl linking group. Also included within the invention are conjugates in which more than one selected moiety is attached to a peptide via a multivalent

5 linking group. One or more proteins can be conjugated together to take advantage of their biophysical and biological properties.

In a still further embodiment, the invention provides conjugates that localize selectively in a particular tissue due to the presence of a targeting agent as a component of the conjugate. In an exemplary embodiment, the targeting agent is a protein. Exemplary

10 proteins include transferrin (brain, blood pool), human serum (HS)-glycoprotein (bone, brain, blood pool), antibodies (brain, tissue with antibody-specific antigen, blood pool), coagulation Factors V-XII (damaged tissue, clots, cancer, blood pool), serum proteins, e.g., α-acid glycoprotein, fetuin, α-fetal protein (brain, blood pool), β2-glycoprotein (liver, atherosclerosis plaques, brain, blood pool), G-CSF, GM-CSF, M-CSF, and EPO (immune

15 stimulation, cancers, blood pool, red blood cell overproduction, neuroprotection), and albumin (increase in half-life).

In addition to the conjugates discussed above, the present invention provides methods for preparing these and other conjugates. Thus, in a further aspect, the invention provides a method of forming a covalent conjugate between a selected moiety and a peptide.

20 Additionally, the invention provides methods for targeting conjugates of the invention to a particular tissue or region of the body.

In exemplary embodiments, the conjugate is formed between a water-soluble polymer, a therapeutic moiety, targeting moiety or a biomolecule, and a glycosylated or non-glycosylated peptide. The polymer, therapeutic moiety or biomolecule is conjugated to the

25 peptide via an intact glycosyl linking group, which is interposed between, and covalently linked to both the peptide and the modifying group (e.g., water-soluble polymer). The method includes contacting the peptide with a mixture containing a modified sugar and a glycosyltransferase for which the modified sugar is a substrate. The reaction is conducted under conditions sufficient to form a covalent bond between the modified sugar and the

30 peptide. The sugar moiety of the modified sugar is preferably selected from nucleotide sugars, activated sugars and sugars, which are neither nucleotides nor activated.

In one embodiment, the invention provides a method for linking two or more peptides through a linking group. The linking group is of any useful structure and may be selected from straight-chain and branched chain structures. Preferably, each terminus of the linker, which is attached to a peptide, includes a modified sugar (i.e., a nascent intact glycosyl

5   linking group).

In an exemplary method of the invention, two peptides are linked together via a linker moiety that includes a PEG linker. The construct conforms to the general structure set forth in the cartoon above. As described herein, the construct of the invention includes two intact glycosyl linking groups (i.e., s + t = 1). The focus on a PEG linker that includes two glycosyl

10   groups is for purposes of clarity and should not be interpreted as limiting the identity of linker arms of use in this embodiment of the invention.

Thus, a PEG moiety is functionalized at a first terminus with a first glycosyl unit and at a second terminus with a second glycosyl unit. The first and second glycosyl units are preferably substrates for different transferases, allowing orthogonal attachment of the first

15   and second peptides to the first and second glycosyl units, respectively. In practice, the (glycosyl)^1-PEG-(glycosyl)^2 linker is contacted with the first peptide and a first transferase for which the first glycosyl unit is a substrate, thereby forming (peptide)^1-(glycosyl)^1-PEG-(glycosyl)^2. The first transferase and/or unreacted peptide is then optionally removed from the reaction mixture. The second peptide and a second transferase

20   for which the second glycosyl unit is a substrate are added to the (peptide)^1-(glycosyl)^1-PEG-(glycosyl)^2 conjugate, forming (peptide)^1-(glycosyl)^1-PEG-(glycosyl)^2-(peptide)^2 . Those of skill in the art will appreciate that the method outlined above is also applicable to forming conjugates between more than two peptides by, for example, the use of a branched PEG, dendrimer, poly(amino acid),

25   polysaccharide or the like.

As noted previously, in an exemplary embodiment, interleukin-2 (IL-2) is conjugated to transferrin via a bifunctional linker that includes an intact glycosyl linking group at each terminus of the PEG moiety (Scheme 1). The IL-2 conjugate has an *in vivo* half-life that is increased over that of IL-2 alone by virtue of the greater molecular size of the conjugate.

30   Moreover, the conjugation of IL-2 to transferrin serves to selectively target the conjugate to the brain. For example, one terminus of the PEG linker is functionalized with a CMP-sialic

acid and the other is functionalized with an UDP-GalNAc. The linker is combined with IL-2 in the presence of a GalNAc transferase, resulting in the attachment of the GalNAc of the linker arm to a serine and/or threonine residue on the IL-2.

In another exemplary embodiment, transferrin is conjugated to a nucleic acid for use in gene therapy.

Scheme 1

1. sialyltransferase
   CMP-SA-PEG-GalNAc-UDP
2. GalNAc transferase
   IL-2
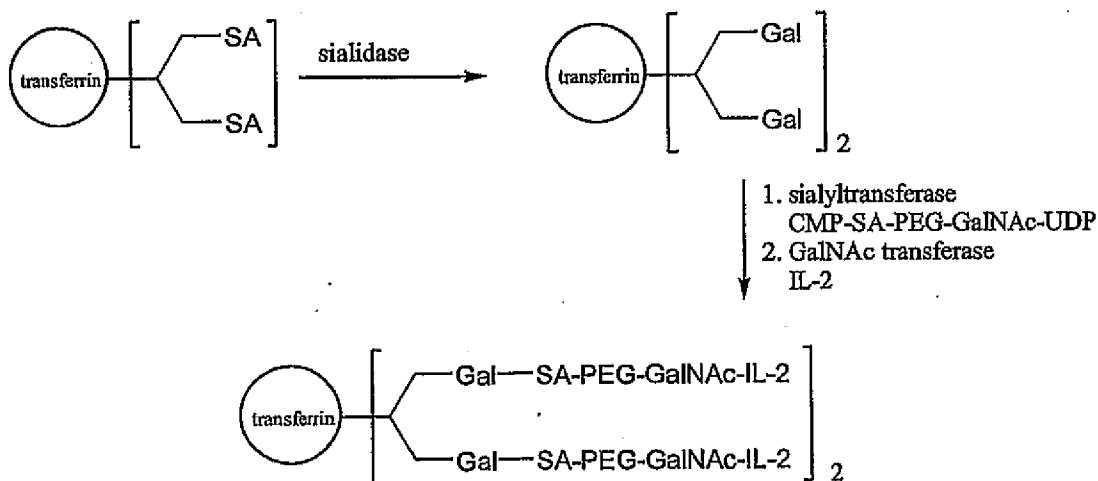
The processes described above can be carried through as many cycles as desired, and is not limited to forming a conjugate between two peptides with a single linker. Moreover, those of skill in the art will appreciate that the reactions functionalizing the intact glycosyl linking groups at the termini of the PEG (or other) linker with the peptide can occur simultaneously in the same reaction vessel, or they can be carried out in a step-wise fashion. When the reactions are carried out in a step-wise manner, the conjugate produced at each step is optionally purified from one or more reaction components (e.g., enzymes, peptides).

A still further exemplary embodiment is set forth in Scheme 2. Scheme 2 shows a method of preparing a conjugate that targets a selected protein, e.g., EPO, to bone and increases the circulatory half-life of the selected protein.

Scheme 2
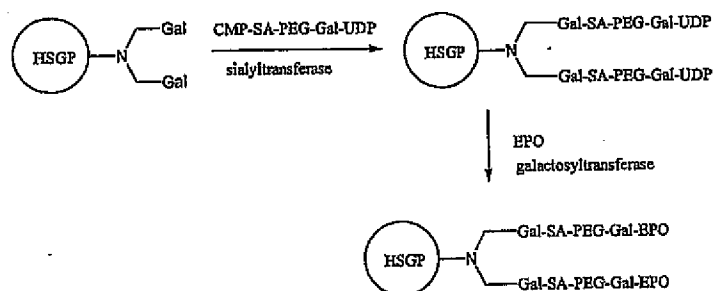
The use of reactive derivatives of PEG (or other linkers) to attach one or more peptide moieties to the linker is within the scope of the present invention. The invention is not

5   limited by the identity of the reactive PEG analogue. Many activated derivatives of poly(ethylene glycol) are available commercially and in the literature. It is well within the abilities of one of skill to choose, and synthesize if necessary, an appropriate activated PEG derivative with which to prepare a substrate useful in the present invention. *See*, Abuchowski *et al. Cancer Biochem. Biophys.*, 7: 175-186 (1984); Abuchowski *et al.*, *J. Biol. Chem.*, 252:

10   3582-3586 (1977); Jackson *et al.*, *Anal. Biochem.*, 165: 114-127 (1987); Koide *et al.*, *Biochem Biophys. Res. Commun.*, 111: 659-667 (1983)), tresylate (Nilsson *et al.*, *Methods Enzymol.*, 104: 56-69 (1984); Delgado *et al.*, *Biotechnol. Appl. Biochem.*, 12: 119-128 (1990)); N-hydroxysuccinimide derived active esters (Buckmann *et al.*, *Makromol. Chem.*, 182: 1379-1384 (1981); Joppich *et al.*, *Makromol. Chem.*, 180: 1381-1384 (1979);

15   Abuchowski *et al.*, *Cancer Biochem. Biophys.*, 7: 175-186 (1984); Katre*et al. Proc. Natl. Acad. Sci. U.S.A.*, 84: 1487-1491 (1987); Kitamura *et al.*, *Cancer Res.*, 51: 4310-4315 (1991); Boccu *et al.*, *Z. Naturforsch.*, 38C: 94-99 (1983), carbonates (Zalipsky *et al.*, POLY(ETHYLENE GLYCOL) CHEMISTRY: BIOTECHNICAL AND BIOMEDICAL APPLICATIONS, Harris, Ed., Plenum Press, New York, 1992, pp. 347-370; Zalipsky *et al.*, *Biotechnol. Appl.*

20   *Biochem.*, 15: 100-114 (1992); Veronese *et al.*, *Appl. Biochem. Biotech.*, 11: 141-152 (1985)), imidazolyl formates (Beauchamp *et al.*, *Anal. Biochem.*, 131: 25-33 (1983); Berger *et al.*, *Blood*, 71: 1641-1647 (1988)), 4-dithiopyridines (Woghiren *et al.*, *Bioconjugate Chem.*, 4: 314-318 (1993)), isocyanates (Byun *et al.*, *ASAIO Journal*, M649-M-653 (1992)) and epoxides (U.S. Pat. No. 4,806,595, issued to Noishiki *et al.*, (1989). Other linking groups

25   include the urethane linkage between amino groups and activated PEG. *See*, Veronese, *et al.*, *Appl. Biochem. Biotechnol.*, 11: 141-152 (1985).

In another exemplary embodiment in which a reactive PEG derivative is utilized, the invention provides a method for extending the blood-circulation half-life of a selected peptide, in essence targeting the peptide to the blood pool, by conjugating the peptide to a synthetic or natural polymer of a size sufficient to retard the filtration of the protein by the

5   glomerulus (e.g., albumin). This embodiment of the invention is illustrated in Scheme 3 in which erythropoietin (EPO) is conjugated to albumin via a PEG linker using a combination of chemical and enzymatic modification.

Scheme 3
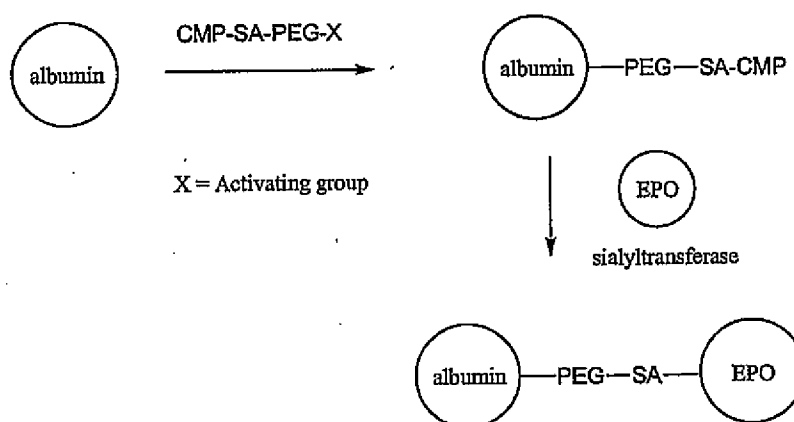
10 .   Thus, as shown in Scheme 3, an amino acid residue of albumin is modified with a reactive PEG derivative, such as X-PEG-(CMP-sialic acid), in which X is an activating group (e.g., active ester, isothiocyanate, etc). The PEG derivative and EPO are combined and contacted with a transferase for which CMP-sialic acid is a substrate. In a further illustrative embodiment, an ε-amine of lysine is reacted with the N-hydroxysuccinimide ester of the

15   PEG-linker to form the albumin conjugate. The CMP-sialic acid of the linker is enzymatically conjugated to an appropriate residue on EPO, e.g., Gal, thereby forming the conjugate. Those of skill will appreciate that the above-described method is not limited to the reaction partners set forth. Moreover, the method can be practiced to form conjugates that include more than two protein moieties by, for example, utilizing a branched linker having

20   more than two termini.

2. Modified Sugars

Modified glycosyl donor species ("modified sugars") are preferably selected from modified sugar nucleotides, activated modified sugars and modified sugars that are simple

saccharides that are neither nucleotides nor activated. Any desired carbohydrate structure can be added to a peptide using the methods of the invention. Typically, the structure will be a monosaccharide, but the present invention is not limited to the use of modified monosaccharide sugars; oligosaccharides and polysaccharides are useful as well.

5   The modifying group is attached to a sugar moiety by enzymatic means, chemical means or a combination thereof, thereby producing a modified sugar. The sugars are substituted at any position that allows for the attachment of the modifying moiety, yet which still allows the sugar to function as a substrate for the enzyme used to ligate the modified sugar to the peptide. In a preferred embodiment, when sialic acid is the sugar, the sialic acid

10   is substituted with the modifying group at either the 9-position on the pyruvyl side chain or at the 5-position on the amine moiety that is normally acetylated in sialic acid.

In certain embodiments of the present invention, a modified sugar nucleotide is utilized to add the modified sugar to the peptide. Exemplary sugar nucleotides that are used in the present invention in their modified form include nucleotide mono-, di- or triphosphates

15   or analogs thereof. In a preferred embodiment, the modified sugar nucleotide is selected from a UDP-glycoside, CMP-glycoside, or a GDP-glycoside. Even more preferably, the modified sugar nucleotide is selected from an UDP-galactose, UDP-galactosamine, UDP-glucose, UDP-glucosamine, GDP-mannose, GDP-fucose, CMP-sialic acid, or CMP-NeuAc. N-acetylamine derivatives of the sugar nucleotides are also of use in the method of the

20   invention.

The invention also provides methods for synthesizing a modified peptide using a modified sugar, e.g., modified-galactose, -fucose, and -sialic acid. When a modified sialic acid is used, either a sialyltransferase or a trans-sialidase (for α2,3-linked sialic acid only) can be used in these methods.

25   In other embodiments, the modified sugar is an activated sugar. Activated modified sugars, which are useful in the present invention are typically glycosides which have been synthetically altered to include an activated leaving group. As used herein, the term "activated leaving group" refers to those moieties, which are easily displaced in enzyme-regulated nucleophilic substitution reactions. Many activated sugars are known in the art.

30   See, for example, Vocadlo et al., In CARBOHYDRATE CHEMISTRY AND BIOLOGY, Vol. 2, Ernst

et al. Ed., Wiley-VCH Verlag: Weinheim, Germany, 2000; Kodama *et al., Tetrahedron Lett.*
34: 6419 (1993); Lougheed, *et al., J. Biol. Chem.* **274**: 37717 (1999)).

5   Examples of activating groups (leaving groups) include fluoro, chloro, bromo,
tosylate ester, mesylate ester, triflate ester and the like. Preferred activated leaving groups,
for use in the present invention, are those that do not significantly sterically encumber the
enzymatic transfer of the glycoside to the acceptor. Accordingly, preferred embodiments of
activated glycoside derivatives include glycosyl fluorides and glycosyl mesylates, with
glycosyl fluorides being particularly preferred. Among the glycosyl fluorides, α-galactosyl
fluoride, α-mannosyl fluoride, α-glucosyl fluoride, α-fucosyl fluoride, α-xylosyl fluoride, α-

10   sialyl fluoride, α-N-acetylglucosaminyl fluoride, α-N-acetylgalactosaminyl fluoride, β-
galactosyl fluoride, β-mannosyl fluoride, β-glucosyl fluoride, β-fucosyl fluoride, β-xylosyl
fluoride, β-sialyl fluoride, β-N-acetylglucosaminyl fluoride and β-N-acetylgalactosaminyl
fluoride are most preferred.

       By way of illustration, glycosyl fluorides can be prepared from the free sugar by first

15   acetylating the sugar and then treating it with HF/pyridine. This generates the
thermodynamically most stable anomer of the protected (acetylated) glycosyl fluoride (*i.e.,*
the α-glycosyl fluoride). If the less stable anomer (*i.e.,* the β-glycosyl fluoride) is desired, it
can be prepared by converting the peracetylated sugar with HBr/HOAc or with HCl to
generate the anomeric bromide or chloride. This intermediate is reacted with a fluoride salt

20   such as silver fluoride to generate the glycosyl fluoride. Acetylated glycosyl fluorides may
be deprotected by reaction with mild (catalytic) base in methanol (*e.g.* NaOMe/MeOH). In
addition, many glycosyl fluorides are commercially available.

       Other activated glycosyl derivatives can be prepared using conventional methods
known to those of skill in the art. For example, glycosyl mesylates can be prepared by

25   treatment of the fully benzylated hemiacetal form of the sugar with mesyl chloride, followed
by catalytic hydrogenation to remove the benzyl groups.

       In a further exemplary embodiment, the modified sugar is an oligosaccharide having
an antennary structure. In a preferred embodiment, one or more of the termini of the
antennae bear the modifying moiety. When more than one modifying moiety is attached to

30   an oligosaccharide having an antennary structure, the oligosaccharide is useful to "amplify"

the modifying moiety; each oligosaccharide unit conjugated to the peptide attaches multiple copies of the modifying group to the peptide. The general structure of a typical chelate of the invention as set forth in the drawing above, encompasses multivalent species resulting from preparing a conjugate of the invention utilizing an antennary structure. Many antennary

5   saccharide structures are known in the art, and the present method can be practiced with them without limitation.

Exemplary modifying groups are discussed below. The modifying groups can be selected for one or more desirable property. Exemplary properties include, but are not limited to, enhanced pharmacokinetics, enhanced pharmacodynamics, improved

10   biodistribution, providing a polyvalent species, improved water solubility, enhanced or diminished lipophilicity, and tissue targeting.

D. Peptide Conjugates

a) Water-Soluble Polymers

The hydrophilicity of a selected peptide is enhanced by conjugation with polar

15   molecules such as amine-, ester-, hydroxyl- and polyhydroxyl-containing molecules. Representative examples include, but are not limited to, polylysine, polyethyleneimine, poly(ethylene glycol) and poly(propyleneglycol). Preferred water-soluble polymers are essentially non-fluorescent, or emit such a minimal amount of fluorescence that they are inappropriate for use as a fluorescent marker in an assay. Polymers that are not naturally

20   occurring sugars may be used. In addition, the use of an otherwise naturally occurring sugar that is modified by covalent attachment of another entity (*e.g.*, poly(ethylene glycol), poly(propylene glycol), poly(aspartate), biomolecule, therapeutic moiety, diagnostic moiety, *etc.*) is also contemplated. In another exemplary embodiment, a therapeutic sugar moiety is conjugated to a linker arm and the sugar-linker arm is subsequently conjugated to a peptide

25   via a method of the invention.

Methods and chemistry for activation of water-soluble polymers and saccharides as well as methods for conjugating saccharides and polymers to various species are described in the literature. Commonly used methods for activation of polymers include activation of functional groups with cyanogen bromide, periodate, glutaraldehyde, biepoxides,

30   epichlorohydrin, divinylsulfone, carbodiimide, sulfonyl halides, trichlorotriazine, *etc. (see*, R. F. Taylor, (1991), PROTEIN IMMOBILISATION. FUNDAMENTALS AND APPLICATIONS, Marcel

Dekker, N.Y.; S. S. Wong, (1992), CHEMISTRY OF PROTEIN CONJUGATION AND CROSSLINKING, CRC Press, Boca Raton; G. T. Hermanson *et al.*, (1993), IMMOBILIZED AFFINITY LIGAND TECHNIQUES, Academic Press, N.Y.; Dunn, R.L., *et al.*, Eds. POLYMERIC DRUGS AND DRUG DELIVERY SYSTEMS, ACS Symposium Series Vol. 469, American

5   Chemical Society, Washington, D.C. 1991).

Routes for preparing reactive PEG molecules and forming conjugates using the reactive molecules are known in the art. For example, U.S. Patent No. 5,672,662 discloses a water soluble and isolatable conjugate of an active ester of a polymer acid selected from linear or branched poly(alkylene oxides), poly(oxyethylated polyols), poly(olefinic alcohols),

10   and poly(acrylomorpholine), wherein the polymer has about 44 or more recurring units.

U.S. Patent No. 6,376,604 sets forth a method for preparing a water-soluble 1-benzotriazolylcarbonate ester of a water-soluble and non-peptidic polymer by reacting a terminal hydroxyl of the polymer with di(1-benzotriazoyl)carbonate in an organic solvent. The active ester is used to form conjugates with a biologically active agent such as a protein

15   or peptide.

WO 99/45964 describes a conjugate comprising a biologically active agent and an activated water soluble polymer comprising a polymer backbone having at least one terminus linked to the polymer backbone through a stable linkage, wherein at least one terminus comprises a branching moiety having proximal reactive groups linked to the branching

20   moiety, in which the biologically active agent is linked to at least one of the proximal reactive groups. Other branched poly(ethylene glycols) are described in WO 96/21469, U.S. Patent No. 5,932,462 describes a conjugate formed with a branched PEG molecule that includes a branched terminus that includes reactive functional groups. The free reactive groups are available to react with a biologically active species, such as a protein or peptide, forming

25   conjugates between the poly(ethylene glycol) and the biologically active species. U.S. Patent No. 5,446,090 describes a bifunctional PEG linker and its use in forming conjugates having a peptide at each of the PEG linker termini.

Conjugates that include degradable PEG linkages are described in WO 99/34833; and WO 99/14259, as well as in U.S. Patent No. 6,348,558. Such degradable linkages are

30   applicable in the present invention.

Although both reactive PEG derivatives and conjugates formed using the derivatives are known in the art, until the present invention, it was not recognized that a conjugate could be formed between PEG (or other polymer) and another species, such as a peptide or glycopeptide, through an intact glycosyl linking group.

5   Many water-soluble polymers are known to those of skill in the art and are useful in practicing the present invention. The term water-soluble polymer encompasses species such as saccharides (e.g., dextran, amylose, hyalouronic acid, poly(sialic acid), heparans, heparins, etc.); poly (amino acids); nucleic acids; synthetic polymers (e.g., poly(acrylic acid), poly(ethers), e.g., poly(ethylene glycol); peptides, proteins, and the like. The present

10   invention may be practiced with any water-soluble polymer with the sole limitation that the polymer must include a point at which the remainder of the conjugate can be attached.

Methods for activation of polymers can also be found in WO 94/17039, U.S. Pat. No. 5,324,844, WO 94/18247, WO 94/04193, U.S. Pat. No. 5,219,564, U.S. Pat. No. 5,122,614, WO 90/13540, U.S. Pat. No. 5,281,698, and more WO 93/15189, and for conjugation

15   between activated polymers and peptides, e.g. Coagulation Factor VIII (WO 94/15625), hemoglobin (WO 94/09027), oxygen carrying molecule (U.S. Pat. No. 4,412,989), ribonuclease and superoxide dismutase (Veronese at al., App. Biochem. Biotech. 11: 141-45 (1985)).

Preferred water-soluble polymers are those in which a substantial proportion of the

20   polymer molecules in a sample of the polymer are of approximately the same molecular weight; such polymers are "homodisperse."

The present invention is further illustrated by reference to a poly(ethylene glycol) conjugate. Several reviews and monographs on the functionalization and conjugation of PEG are available. See, for example, Harris, Macronol. Chem. Phys. C25: 325-373 (1985);

25   Scouten, Methods in Enzymology 135: 30-65 (1987); Wong et al., Enzyme Microb. Technol. 14: 866-874 (1992); Delgado et al., Critical Reviews in Therapeutic Drug Carrier Systems 9: 249-304 (1992); Zalipsky, Bioconjugate Chem. 6: 150-165 (1995); and Bhadra, et al., Pharmazie, 57:5-29 (2002).

Poly(ethylene glycol) molecules suitable for use in the invention include, but are not

30   limited to, those described by the following Formula 3:

Formula 3.

R= H, alkyl, benzyl, aryl, acetal, OHC-, $H_2N-CH_2CH_2-$, $HS-CH_2CH_2-$,

, -sugar-nucleotide, protein, methyl, ethyl;
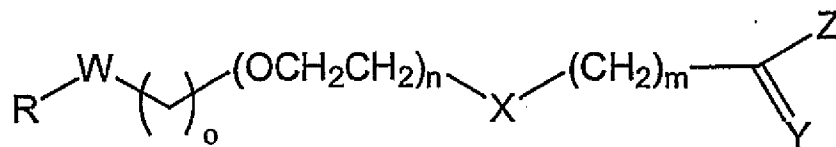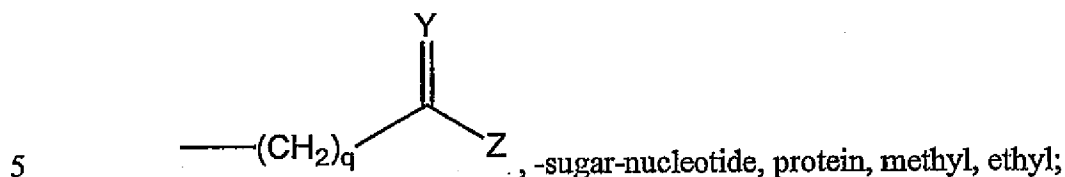
X, Y, W, U (independently selected) = O, S, NH, N-R';
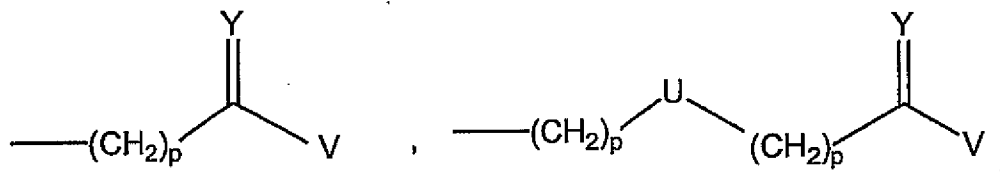
R', R''' (independently selected) = alkyl, benzyl, aryl, alkyl aryl, pyridyl, substituted aryl, arylalkyl, acylaryl;

n = 1 to 2000;
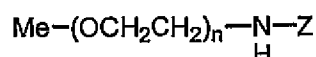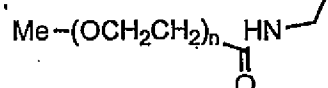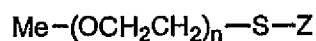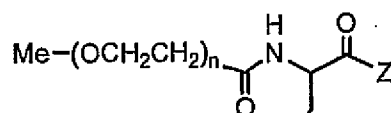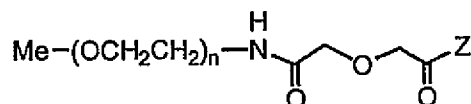
m, q, p (independently selected) = 0 to 20

o = 0 to 20;

Z = HO, NH_2, halogen, S-R''', activated esters,

-sugar-nucleotide, protein, imidazole, HOBT, tetrazole, halide; and

V = HO, NH_2, halogen, S-R''', activated esters, activated amides, -sugar-nucleotide, protein.

In preferred embodiments, the poly(ethylene glycol) molecule is selected from the following:

$Me-(OCH_2CH_2)_n-O$ —— Z (O)

$Me-(OCH_2CH_2)_n-O$ —— Z (O)

$Me-(OCH_2CH_2)_n-O$ —— Z (O)

$Me-(OCH_2CH_2)_n-N$ —— O —— Z (H, O)

$Me-(OCH_2CH_2)_n-O$ —— Z (O)

$Me-(OCH_2CH_2)_n$ —— Z (H, N, O)

$Me-(OCH_2CH_2)_n$ HN (O)

$Me-(OCH_2CH_2)_n-S-Z$

$Me-(OCH_2CH_2)_n-N-Z$
                  H
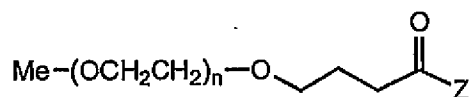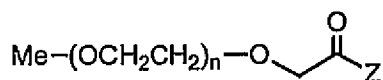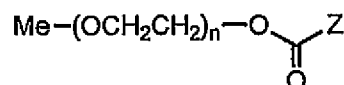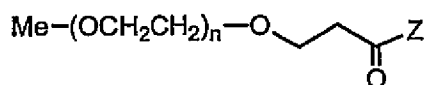
The poly(ethylene glycol) useful in forming the conjugate of the invention is either linear or branched. Branched poly(ethylene glycol) molecules suitable for use in the invention include, but are not limited to, those described by the following Formula:

Formula 4:

$$R''-W(\quad)_m(OCH_2CH_2)_n-X_{(CH_2)_q}$$
$$R'-A(\quad)_o(OCH_2CH_2)_p-B \quad Z \quad Y$$
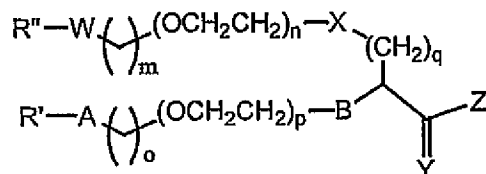
5

R', R'', R''' (independently selected) = H, alkyl, benzyl, aryl, acetal, OHC-, $H_2N-CH_2CH_2$-,

$HS-CH^2CH_2$-, $-(CH_2)_qCY-Z$, -sugar-nucleotide, protein, methyl, ethyl, heteroaryl,

acylalkyl, acylaryl, acylalkylaryl;

X, Y, W, A, B (independently selected) = O, S, NH, N-R', $(CH_2)_i$;

10   n, p (independently selected) = 1 to 2000;

m, q, o (independently selected) = 0 to 20;

Z = HO, NH_2, halogen, S-R''', activated esters,

$$—(CH_2)_p \quad V \quad (Y)$$
$$, \quad —(CH_2)_p \quad U \quad (CH_2)_p \quad V \quad (Y) \quad ,$$
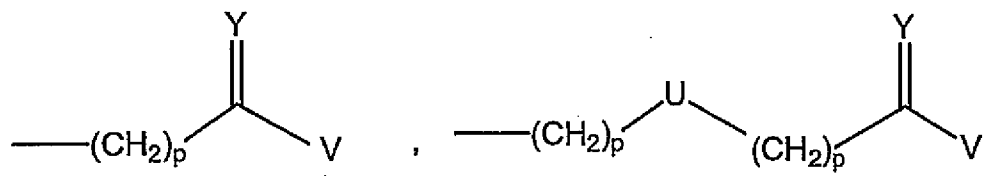
-sugar-nucleotide, protein;

15   V = HO, NH_2, halogen, S-R''', activated esters, activated amides,

-sugar-nucleotide, protein.

The *in vivo* half-life, area under the curve, and/or residence time of therapeutic peptides can also be enhanced with water-soluble polymers such as polyethylene glycol (PEG) and polypropylene glycol (PPG). For example, chemical modification of proteins with PEG (PEGylation) increases their molecular size and decreases their surface- and functional

5   group-accessibility, each of which are dependent on the size of the PEG attached to the protein. This results in an improvement of plasma half-lives and in proteolytic-stability, and a decrease in immunogenicity and hepatic uptake (Chaffee *et al. J. Clin. Invest.* 89: 1643-1651 (1992); Pyatak *et al. Res. Commun. Chem. Pathol Pharmacol.* 29: 113-127 (1980)). PEGylation of interleukin-2 has been reported to increase its antitumor potency *in vivo* (Katre

10   *et al. Proc. Natl. Acad. Sci. USA.* 84: 1487-1491 (1987)) and PEGylation of a F(ab')2 derived from the monoclonal antibody A7 has improved its tumor localization (Kitamura *et al. Biochem. Biophys. Res. Commun.* 28: 1387-1394 (1990)).

In one preferred embodiment, the *in vivo* half-life of a peptide derivatized with a water-soluble polymer by a method of the invention is increased relevant to the *in vivo* half-

15   life of the non-derivatized peptide. In another preferred embodiment, the area under the curve of a peptide derivatized with a water-soluble polymer using a method of the invention is increased relevant to the area under the curve of the non-derivatized peptide. In another preferred embodiment, the residence time of a peptide derivatized with a water-soluble polymer using a method of the invention is increased relevant to the residence time of the

20   non-derivatized peptide. Techniques to determine the *in vivo* half-life, the area under the curve and the residence time are well known in the art. Descriptions of such techniques can be found in J.G. Wagner, 1993, Pharmacokinetics for the Pharmaceutical Scientist, Technomic Publishing Company, Inc. Lancaster PA.

The increase in peptide *in vivo* half-life is best expressed as a range of percent

25   increase in this quantity. The lower end of the range of percent increase is about 40%, about 60%, about 80%, about 100%, about 150% or about 200%. The upper end of the range is about 60%, about 80%, about 100%, about 150%, or more than about 250%.

In an exemplary embodiment, the present invention provides a PEGylated follicle stimulating hormone (Examples 9 and 10). In a further exemplary embodiment, the invention

30   provides a PEGylated transferrin (Example 13).

Other exemplary water-soluble polymers of use in the invention include, but are not limited to linear or branched poly(alkylene oxides), poly(oxyethylated polyols), poly(olefinic alcohols), and poly(acrylomorpholine), dextran, starch, poly(amino acids), etc.

b) Water-insoluble polymers

5   The conjugates of the invention may also include one or more water-insoluble polymers. This embodiment of the invention is illustrated by the use of the conjugate as a vehicle with which to deliver a therapeutic peptide in a controlled manner. Polymeric drug delivery systems are known in the art. See, for example, Dunn et al., Eds. POLYMERIC DRUGS AND DRUG DELIVERY SYSTEMS, ACS Symposium Series Vol. 469, American

10   Chemical Society, Washington, D.C. 1991. Those of skill in the art will appreciate that substantially any known drug delivery system is applicable to the conjugates of the present invention.

Representative water-insoluble polymers include, but are not limited to, polyphosphazines, poly(vinyl alcohols), polyamides, polycarbonates, polyalkylenes,

15   polyacrylamides, polyalkylene glycols, polyalkylene oxides, polyalkylene terephthalates, polyvinyl ethers, polyvinyl esters, polyvinyl halides, polyvinylpyrrolidone, polyglycolides, polysiloxanes, polyurethanes, poly(methyl methacrylate), poly(ethyl methacrylate), poly(butyl methacrylate), poly(isobutyl methacrylate), poly(hexyl methacrylate), poly(isodecyl methacrylate), poly(lauryl methacrylate), poly(phenyl methacrylate),

20   poly(methyl acrylate), poly(isopropyl acrylate), poly(isobutyl acrylate), poly(octadecyl acrylate) polyethylene, polypropylene, poly(ethylene glycol), poly(ethylene oxide), poly (ethylene terephthalate), poly(vinyl acetate), polyvinyl chloride, polystyrene, polyvinyl pyrrolidone, pluronics and polyvinylphenol and copolymers thereof.

Synthetically modified natural polymers of use in conjugates of the invention include,

25   but are not limited to, alkyl celluloses, hydroxyalkyl celluloses, cellulose ethers, cellulose esters, and nitrocelluloses. Particularly preferred members of the broad classes of synthetically modified natural polymers include, but are not limited to, methyl cellulose, ethyl cellulose, hydroxypropyl cellulose, hydroxypropyl methyl cellulose, hydroxybutyl methyl cellulose, cellulose acetate, cellulose propionate, cellulose acetate butyrate, cellulose

30   acetate phthalate, carboxymethyl cellulose, cellulose triacetate, cellulose sulfate sodium salt, and polymers of acrylic and methacrylic esters and alginic acid.

Cohn *et al.*, U.S. Patent No. 4,826,945). These copolymers are not crosslinked and are water-soluble so that the body can excrete the degraded block copolymer compositions. *See*, Younes *et al.*, *J Biomed. Mater. Res.* **21**: 1301-1316 (1987); and Cohn *et al.*, *J Biomed. Mater. Res.* **22**: 993-1009 (1988).

5   Presently preferred bioresorbable polymers include one or more components selected from poly(esters), poly(hydroxy acids), poly(lactones), poly(amides), poly(ester-amides), poly (amino acids), poly(anhydrides), poly(orthoesters), poly(carbonates), poly(phosphazines), poly(phosphoesters), poly(thioesters), polysaccharides and mixtures thereof. More preferably still, the biosresorbable polymer includes a poly(hydroxy) acid

10   component. Of the poly(hydroxy) acids, polylactic acid, polyglycolic acid, polycaproic acid, polybutyric acid, polyvaleric acid and copolymers and mixtures thereof are preferred.

In addition to forming fragments that are absorbed *in vivo* ("bioresorbed"), preferred polymeric coatings for use in the methods of the invention can also form an excretable and/or metabolizable fragment.

15   Higher order copolymers can also be used in the present invention. For example, Casey *et al.*, U.S. Patent No. 4,438,253, which issued on March 20, 1984, discloses tri-block copolymers produced from the transesterification of poly(glycolic acid) and an hydroxyl-ended poly(alkylene glycol). Such compositions are disclosed for use as resorbable monofilament sutures. The flexibility of such compositions is controlled by the incorporation

20   of an aromatic orthocarbonate, such as tetra-p-tolyl orthocarbonate into the copolymer structure.

Other coatings based on lactic and/or glycolic acids can also be utilized. For example, Spinu, U.S. Patent No. 5,202,413, which issued on April 13, 1993, discloses biodegradable multi-block copolymers having sequentially ordered blocks of polylactide and/or

25   polyglycolide produced by ring-opening polymerization of lactide and/or glycolide onto either an oligomeric diol or a diamine residue followed by chain extension with a di-functional compound, such as, a diisocyanate, diacylchloride or dichlorosilane.

Bioresorbable regions of coatings useful in the present invention can be designed to be hydrolytically and/or enzymatically cleavable. For purposes of the present invention,

30   "hydrolytically cleavable" refers to the susceptibility of the copolymer, especially the bioresorbable region, to hydrolysis in water or a water-containing environment. Similarly,

polysaccharides, polyurethane hydrogel, polyurethane-urea hydrogel and combinations thereof are presently preferred.

In yet another exemplary embodiment, the conjugate of the invention includes a component of a liposome. Liposomes can be prepared according to methods known to those

5   skilled in the art, for example, as described in Eppstein *et al.*, U.S. Patent No. 4,522,811, which issued on June 11, 1985. For example, liposome formulations may be prepared by dissolving appropriate lipid(s) (such as stearoyl phosphatidyl ethanolamine, stearoyl phosphatidyl choline, arachadoyl phosphatidyl choline, and cholesterol) in an inorganic solvent that is then evaporated, leaving behind a thin film of dried lipid on the surface of the

10   container. An aqueous solution of the active compound or its pharmaceutically acceptable salt is then introduced into the container. The container is then swirled by hand to free lipid material from the sides of the container and to disperse lipid aggregates, thereby forming the liposomal suspension.

The above-recited microparticles and methods of preparing the microparticles are

15   offered by way of example and they are not intended to define the scope of microparticles of use in the present invention. It will be apparent to those of skill in the art that an array of microparticles, fabricated by different methods, are of use in the present invention.

c) Biomolecules

In another preferred embodiment, the modified sugar bears a biomolecule. In still

20   further preferred embodiments, the biomolecule is a functional protein, enzyme, antigen, antibody, peptide, nucleic acid (*e.g.*, single nucleotides or nucleosides, oligonucleotides, polynucleotides and single- and higher-stranded nucleic acids), lectin, receptor or a combination thereof.

Some preferred biomolecules are essentially non-fluorescent, or emit such a minimal

25   amount of fluorescence that they are inappropriate for use as a fluorescent marker in an assay. Other biomolecules may be fluorescent. The use of an otherwise naturally occurring sugar that is modified by covalent attachment of another entity (*e.g.*, PEG, biomolecule, therapeutic moiety, diagnostic moiety, *etc.*) is appropriate. In an exemplary embodiment, a sugar moiety, which is a biomolecule, is conjugated to a linker arm and the sugar-linker arm cassette is

30   subsequently conjugated to a peptide via a method of the invention.

Neuroimmunol., **64(1)**:91-100 (1996); Schmidt, J., *J. Neurosci. Res.*, **65(1)**:59-67 (2001);
Wender, *et al.*, *Folia Neuropathol.*, **39(2)**:91-93 (2001); Martin, *et al.*, *Springer Semin.*
Immunopathol., **18(1)**:1-24 (1996); Takane, *et al.*, *J. Pharmacol. Exp. Ther.*, **294(2)**:746-752
(2000); Sburlati, *et al.*, *Biotechnol. Prog.*, **14**:189-192 (1998); Dodd, *et al.*, *Biochimica et*
5   *Biophysica Acta*, **787**:183-187 (1984); Edelbaum, *et al.*, *J. Interferon Res.*, **12**:449-453
(1992); Conradt, *et al.*, *J. Biol. Chem.*, **262(30)**:14600-14605 (1987); Civas, *et al.*, *Eur. J.*
Biochem., **173**:311-316 (1988); Demolder, *et al.*, *J. Biotechnol.*, **32**:179-189 (1994); Sedmak,
et al., *J. Interferon Res.*, **9(Suppl 1)**:S61-S65 (1989); Kagawa, *et al.*, *J. Biol. Chem.*,
263(33):17508-17515 (1988); Hershenson, *et al.*, U.S. Patent No. 4,894,330; Jayaram, *et al.*,
10   *J. Interferon Res.*, **3(2)**:177-180 (1983); Menge, *et al.*, *Develop. Biol. Standard.*, **66**:391-401
(1987); Vonk, *et al.*, *J. Interferon Res.*, **3(2)**:169-175 (1983); and Adolf, *et al.*, *J. Interferon*
Res., **10**:255-267 (1990). For references relevant to interferon-α, *see*, Asano, *et al.*, *Eur. J.*
Cancer, **27(Suppl 4)**:S21-S25 (1991); Nagy, *et al.*, *Anticancer Research*, **8(3)**:467-470
(1988); Dron, *et al.*, *J. Biol. Regul. Homeost. Agents*, **3(1)**:13-19 (1989); Habib, *et al.*, *Am.*
15   *Surg.*, **67(3)**:257-260 (3/2001); and Sugyiama, *et al.*, *Eur. J. Biochem.*, **217**:921-927 (1993).

In an exemplary interferon conjugate, interferon β is conjugated to a second peptide
via a linker arm. The linker arm includes an intact glycosyl linking group through which it is
attached to the second peptide via a method of the invention. The linker arm also optionally
includes a second intact glycosyl linking group, through which it is attached to the interferon.

20   In another exemplary embodiment, the invention provides a conjugate of follicle
stimulating hormone (FSH). FSH is a glycoprotein hormone. *See*, for example, Saneyoshi,
et al., *Biol. Reprod.*, **65**:1686-1690 (2001); Hakola, *et al.*, *J. Endocrinol.*, **158**:441-448
(1998); Stanton, *et al.*, *Mol. Cell. Endocrinol.*, **125**:133-141 (1996); Walton, *et al.*, *J. Clin.*
Endocrinol. Metab., **86(8)**:3675-3685 (08/2001); Ulloa-Aguirre, *et al.*, *Endocrine*, **11(3)**:205-
25   215 (12/1999); Castro-Fernández, *et al.I*, *J. Clin. Endocrinol. Matab.*, **85(12)**:4603-4610
(2000); Prevost, Rebecca R., *Pharmacotherapy*, **18(5)**:1001-1010 (1998); Linskens, *et al.*,
The FASEB Journal, **13**:639-645 (04/1999); Butnev, *et al.*, *Biol. Reprod.*, **58**:458-469 (1998);
Muyan, *et al.*, *Mol. Endo.*, **12(5)**:766-772 (1998); Min, *et al.*, *Endo. J.*, **43(5)**:585-593 (1996);
· Boime, *et al.*, *Recent Progress in Hormone Research*, **34**:271-289 (1999); and Rafferty, *et al.*,
30   *J. Endo.*, **145**:527-533 (1995). The FSH conjugate can be formed in a manner similar to that
described for interferon.

melanotransferrin (p97), ceruloplasmin, and divalent cation transporter. Contemplated

linkages include, but are not limited to, protein-sugar-linker-sugar-protein, protein-sugar-

linker-protein and multivalent forms thereof, and protein-sugar-linker-drug where the drug

includes small molecules, peptides, lipids, among others.

5   Site-specific and target-oriented delivery of therapeutic agents is desirable for the

purpose of treating a wide variety of human diseases, such as different types of malignancies

and certain neurological disorders. Such procedures are accompanied by fewer side effects

and a higher efficiacy of drug. Various principles have been relied on in designing these

delivery systems. For a review, *see* Garnett, *Advanced Drug Delivery Reviews* 53:171-216

10   (2001).

One important consideration in designing a drug delivery system to target tissues

specifically. The discovery of tumor surface antigens has made it possible to develop

therapeutic approaches where tumor cells displaying definable surface antigens are

specifically targeted and killed. There are three main classes of therapeutic monoclonal

15   antibodies (MAb) that have demonstrated effectiveness in human clinical trials in treating

malignancies: (1) unconjugated MAb, which either directly induces growth inhibition and/or

apoptosis, or indirectly activates host defense mechanisms to mediate antitumor cytotoxicity;

(2) drug-conjugated MAb, which preferentially delivers a potent cytotoxic toxin to the tumor

cells and therefore minimizes the systemic cytotoxicity commonly associated with

20   conventional chemotherapy; and (3) radioisotope-conjugated MAb, which delivers a

sterilizing dose of radiation to the tumor. See review by Reff et al., *Cancer Control* 9:152-

166 (2002).

In order to arm MAbs with the power to kill malignant cells, the MAbs can be

connected to a toxin, which may be obtained from a plant, bacterial, or fungal source, to form

25   chimeric proteins called immunotoxins. Frequently used plant toxins are divided into two

classes: (1) holotoxins (or class II ribosome inactivating proteins), such as ricin, abrin,

mistletoe lectin, and modeccin, and (2) hemitoxins (class I ribosome inactivating proteins),

such as pokeweed antiviral protein (PAP), saporin, Bryodin 1, bouganin, and gelonin.

Commonly used bacterial toxins include diphtheria toxin (DT) and Pseudomonas exotoxin

30   (PE). Kreitman, *Current Pharmaceutical Biotechnology* 2:313-325 (2001).

Conventional immunotoxins contain an MAb chemically conjugated to a toxin that is mutated or chemically modified to minimized binding to normal cells. Examples include anti-B4-blocked ricin, targeting CD5; and RFB4-deglycosylated ricin A chain, targeting CD22. Recombinant immunotoxins developed more recently are chimeric proteins

5   consisting of the variable region of an antibody directed against a tumor antigen fused to a protein toxin using recombinant DNA technology. The toxin is also frequently genetically modified to remove normal tissue binding sites but retain its cytotoxicity. A large number of differentiation antigens, overexpressed receptors, or cancer-specific antigens have been identified as targets for immunotoxins, *e.g.*, CD19, CD22, CD20, IL-2 receptor (CD25),

10   CD33, IL-4 receptor, EGF receptor and its mutants, ErB2, Lewis carbohydrate, mesothelin, transferrin receptor, GM-CSF receptor, Ras, Bcr-Abl, and c-Kit, for the treatment of a variety of malignancies including hematopoietic cancers, glioma, and breast, colon, ovarian, bladder, and gastrointestinal cancers. *See e.g.*, Brinkmann et al., *Expert Opin. Biol. Ther.* 1:693-702 (2001); Perentesis and Sievers, *Hematology/Oncology Clinics of North America* 15:677-701

15   (2001).

    MAbs conjugated with radioisotope are used as another means of treating human malignancies, particularly hematopoietic malignancies, with a high level of specificity and effectiveness. The most commonly used isotopes for therapy are the high-energy -emitters, such as ^{131}I and ^{90}Y. Recently, ^{213}Bi-labeled anti-CD33 humanized MAb has also been tested

20   in phase I human clinical trials. Reff et al., *supra*.

    A number of MAbs have been used for therapeutic purposes. For example, the use of rituximab (Rituxan™), a recombinant chimeric anti-CD20 MAb, for treating certain hematopoietic malignancies was approved by the FDA in 1997. Other MAbs that have since been approved for therapeutic uses in treating human cancers include: alemtuzumab

25   (Campath-1H™), a humanized rat antibody against CD52; and gemtuzumab ozogamicin (Mylotarg™), a calicheamicin-conjugated humanized mouse antCD33 MAb. The FDA is also currently examining the safety and efficacy of several other MAbs for the purpose of site-specific delivery of cytotoxic agents or radiation, *e.g.*, radiolabeled Zevalin™ and Bexxar™. Reff et al., *supra*.

30   A second important consideration in designing a drug delivery system is the accessibility of a target tissue to a therapeutic agent. This is an issue of particular concern in

the case of treating a disease of the central nervous system (CNS), where the blood-brain barrier prevents the diffusion of macromolecules. Several approaches have been developed to bypass the blood-brain barrier for effective delivery of therapeutic agents to the CNS.

The understanding of iron transport mechanism from plasma to brain provides a

5   useful tool in bypassing the blood-brain barrier (BBB). Iron, transported in plasma by transferrin, is an essential component of virtually all types of cells. The brain needs iron for metabolic processes and receives iron through transferrin receptors located on brain capillary endothelial cells via receptor-mediated transcytosis and endocytosis. Moos and Morgan, *Cellular and Molecular Neurobiology* 20:77-95 (2000). Delivery systems based on

10   transferrin-transferrin receptor interaction have been established for the efficient delivery of peptides, proteins, and liposomes into the brain. For example, peptides can be coupled with a Mab directed against the transferrin receptor to achieve greater uptake by the brain, Moos and Morgan, *Supra*. Similarly, when coupled with an MAb directed against the transferrin receptor, the transportation of basic fibroblast growth factor (bFGF) across the blood-brain

15   barrier is enhanced. Song et al., *The Journal of Pharmacology and Experimental Therapeutics* 301:605-610 (2002); Wu et al., *Journal of Drug Targeting* 10:239-245 (2002). In addition, a liposomal delivery system for effective transport of the chemotherapy drug, doxorubicin, into C6 glioma has been reported, where transferrin was attached to the distal ends of liposomal PEG chains. Eavarone et al., *J. Biomed. Mater. Res.* 51:10-14 (2000). A

20   number of US patents also relate to delivery methods bypassing the blood-brain barrier based on transferrin-transferrin receptor interaction. *See e.g.*, US Patent Nos. 5,154,924; 5,182,107; 5,527,527; 5,833,988; 6,015,555.

There are other suitable conjugation partners for a pharmaceutical agent to bypass the blood-brain barrier. For example, US Patent Nos. 5,672,683, 5,977,307 and WO 95/02421

25   relate to a method of delivering a neuropharmaceutical agent across the blood-brain barrier, where the agent is administered in the form of a fusion protein with a ligand that is reactive with a brain capillary endothelial cell receptor; WO 99/00150 describes a drug delivery system in which the transportation of a drug across the blood-brain barrier is facilitated by conjugation with an MAb directed against human insulin receptor; WO 89/10134 describes a

30   chimeric peptide, which includes a peptide capable of crossing the blood brain barrier at a relatively high rate and a hydrophilic neuropeptide incapable of transcytosis, as a means of

lysosomes which have an acidic pH. Once internalized into the endosome or lysosome, the linker is hydrolyzed and the therapeutic agent is released from the targeting agent.

In an exemplary embodiment, transferrin is conjugated via a linker to an enzyme desired to be targeted to a cell that presents transferrin receptors in a patient. The patient

5   could, for example, require enzyme replacement therapy for that particular enzyme. In particularly preferred embodiments, the enzyme is one that is lacking in a patient with a lysosomal storage disease (see Table 4). Once in circulation, the transferrin-enzyme conjugate binds to transferrin receptors and is internalized in early endosomes (Xing et al., 1998, Biochem. J. 336:667; Li et al., 2002, Trends in Pharmcol. Sci. 23:206; Suhaila et al.,

10   1998, J. Biol. Chem. 273:14355). Other contemplated targeting agents that are related to transferrin include, but are not limited to, lactotransferrin (lactoferrin), melanotransferrin (p97), ceruloplasmin, and divalent cation transporter.

In another exemplary embodiment, tranferrin-dystrophin conjugates would enter endosomes by the transferrin pathway. Once there, the dystrophin is released due to a

15   hydrolysable linker which can then be taken to the intracellular compartment where it is required. This embodiment may be used to treat a patient with muscular dystrophy by supplementing a genetically defective dystrophin gene and/or protein with the functional dystrophin peptide connected to the transferrin.

20   E. Therapeutic Moieties

In another preferred embodiment, the modified sugar includes a therapeutic moiety. Those of skill in the art will appreciate that there is overlap between the category of therapeutic moieties and biomolecules; many biomolecules have therapeutic properties or potential.

25   The therapeutic moieties can be agents already accepted for clinical use or they can be drugs whose use is experimental, or whose activity or mechanism of action is under investigation. The therapeutic moieties can have a proven action in a given disease state or can be only hypothesized to show desirable action in a given disease state. In a preferred embodiment, the therapeutic moieties are compounds, which are being screened for their

30   ability to interact with a tissue of choice. Therapeutic moieties, which are useful in practicing the instant invention include drugs from a broad range of drug classes having a variety of

lineomycin, methacycline, methenamine, minocycline, neomycin, netilmycin, paromomycin, streptomycin, tobramycin, miconazole and amantadine.

Other drug moieties of use in practicing the present invention include antineoplastic drugs (*e.g.*, antiandrogens (*e.g.*, leuprolide or flutamide), cytocidal agents (*e.g.*, adriamycin,

5   doxorubicin, taxol, cyclophosphamide, busulfan, cisplatin, β-2-interferon) anti-estrogens (*e.g.*, tamoxifen), antimetabolites (*e.g.*, fluorouracil, methotrexate, mercaptopurine, thioguanine). Also included within this class are radioisotope-based agents for both diagnosis and therapy, and conjugated toxins, such as ricin, geldanamycin, mytansin, CC-1065, C-1027, the duocarmycins, calicheamycin and related structures and analogues thereof.

10 The therapeutic moiety can also be a hormone (*e.g.*, medroxyprogesterone, estradiol, leuprolide, megestrol, octreotide or somatostatin); muscle relaxant drugs (*e.g.*, cinnamedrine, cyclobenzaprine, flavoxate, orphenadrine, papaverine, mebeverine, idaverine, ritodrine, diphenoxylate, dantrolene and azumolen); antispasmodic drugs; bone-active drugs (*e.g.*, diphosphonate and phosphonoalkylphosphinate drug compounds); endocrine modulating

15 drugs (*e.g.*, contraceptives (*e.g.*, ethinodiol, ethinyl estradiol, norethindrone, mestranol, desogestrel, medroxyprogesterone), modulators of diabetes (*e.g.*, glyburide or chlorpropamide), anabolics, such as testolactone or stanozolol, androgens (*e.g.*, methyltestosterone, testosterone or fluoxymesterone), antidiuretics (*e.g.*, desmopressin) and calcitonins).

20 Also of use in the present invention are estrogens (*e.g.*, diethylstilbesterol), glucocorticoids (*e.g.*, triamcinolone, betamethasone, etc.) andprogesterones, such as norethindrone, ethynodiol, norethindrone, levonorgestrel; thyroid agents (*e.g.*, liothyronine or levothyroxine) or anti-thyroid agents (*e.g.*, methimazole); antihyperprolactinemic drugs (*e.g.*, cabergoline); hormone suppressors (*e.g.*, danazol or goserelin), oxytocics (*e.g.*,

25 methylergonovine or oxytocin) and prostaglandins, such as mioprostol, alprostadil or dinoprostone, can also be employed.

Other useful modifying groups include immunomodulating drugs (*e.g.*, antihistamines, mast cell stabilizers, such as lodoxamide and/or cromolyn, steroids (*e.g.*, triamcinolone, beclomethazone, cortisone, dexamethasone, prednisolone,

30 methylprednisolone, beclomethasone, or clobetasol), histamine H2 antagonists (*e.g.*, famotidine, cimetidine, ranitidine), immunosuppressants (*e.g.*, azathioprine, cyclosporin), etc.

manner analogous to that set forth using sialic acid as an example. For example, numerous

methods are available for modifying galactose, glucose, N-acetylgalactosamine and fucose to

name a few sugar substrates, which are readily modified by art recognized methods. *See*, for

example, Elhalabi *et al.*, *Curr. Med. Chem.* **6**: 93 (1999); and Schafer *et al.*, *J. Org. Chem.*

5   **65**: 24 (2000).

In an exemplary embodiment, the peptide that is modified by a method of the

invention is a peptide that is produced in mammalian cells (e.g., CHO cells) or in a transgenic

animal and thus, contains N- and/or O-linked oligosaccharide chains, which are incompletely

sialylated. The oligosaccharide chains of the glycopeptide lacking a sialic acid and

10   containing a terminal galactose residue can be PEGylated, PPGylated or otherwise modified

with a modified sialic acid.

In Scheme 4, the mannosamine glycoside **1**, is treated with the active ester of a

protected amino acid (*e.g.*, glycine) derivative, converting the sugar amine residue into the

corresponding protected amino acid amide adduct. The adduct is treated with an aldolase to

15   form the sialic acid **2**. Compound **2** is converted to the corresponding CMP derivative by the

action of CMP-SA synthetase, followed by catalytic hydrogenation of the CMP derivative to

produce compound **3**. The amine introduced via formation of the glycine adduct is utilized as

a locus of PEG or PPG attachment by reacting compound **3** with an activated PEG or PPG

derivative (*e.g.*, PEG-C(O)NHS, PPG-C(O)NHS), producing 4 or 5, respectively.

20   **Scheme 4**

CMP-SA-5-NHCOCH$_2$NH—**PEG**

CMP-SA-5-NHCOCH$_2$NH—**PPG**

CMP-SA-5-NHCOCH$_2$NH$_2$

5
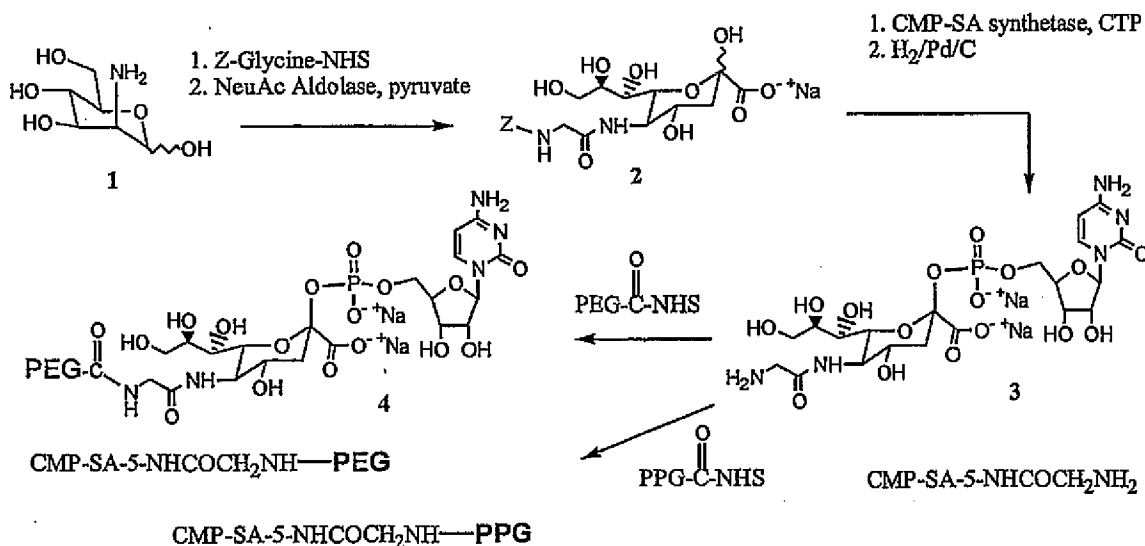
Table 2 sets forth representative examples of sugar monophosphates that are derivatized with a PEG or PPG moiety. Certain of the compounds of Table 2 are prepared by the method of Scheme 1. Other derivatives are prepared by art-recognized methods. *See*, for example, Keppler *et al.*, *Glycobiology* 11: 11R (2001); and Charter *et al.*, *Glycobiology* 10: 1049 (2000)). Other amine reactive PEG and PPG analogues are commercially available, or they can be prepared by methods readily accessible to those of skill in the art.

Table 2: Examples of sugar monophosphates that are derivatized with a PEG or PPG moiety
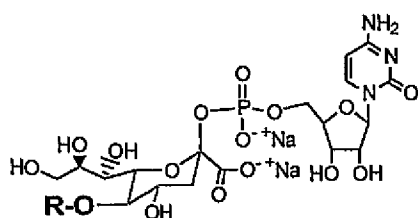
CMP-KDN-5-O-R
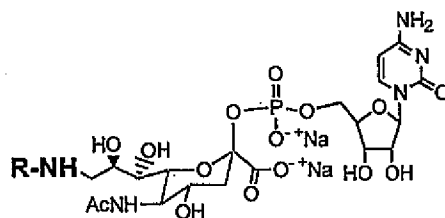
CMP-NeuAc-9-NH-R
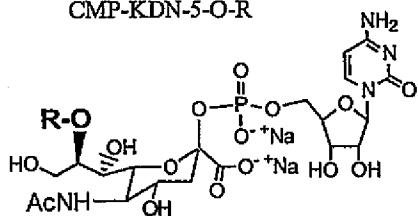
CMP-NeuAc-8-O-R
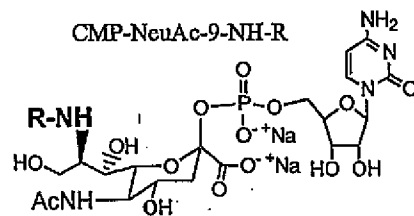
CMP-NeuAc-8-NH-R
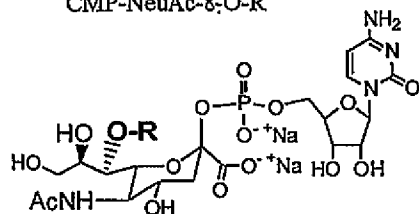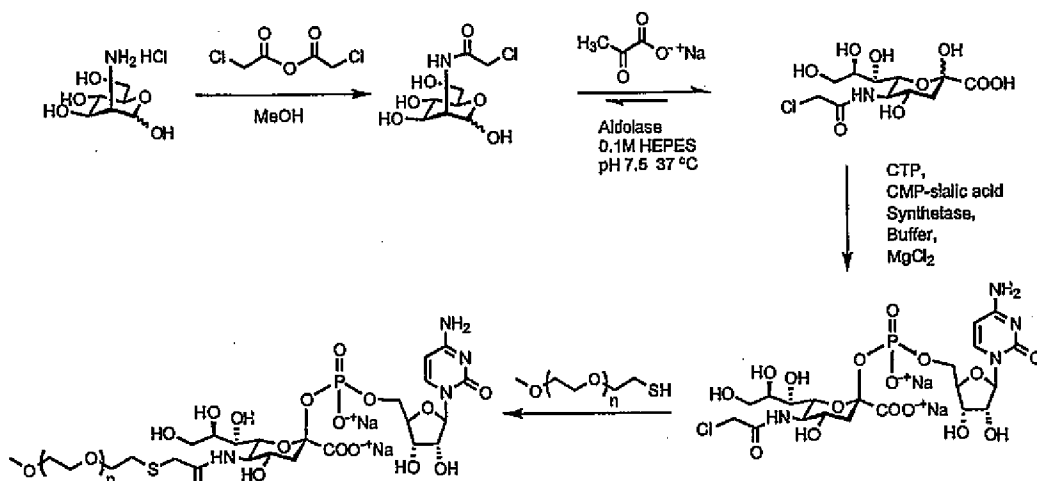
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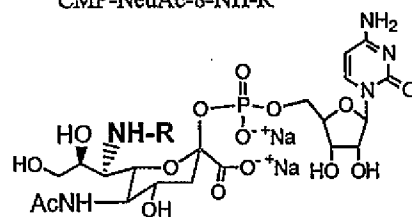
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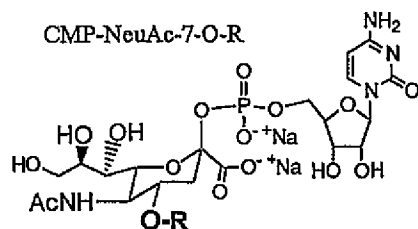
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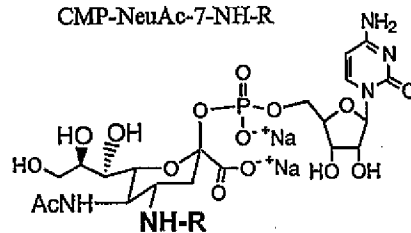
CMP-NeuAc-4-NH-R

Scheme 5

The resulting chloro-derivatized glycan is contacted with pyruvate in the presence of an aldolase, forming a chloro-derivatized sialic acid. The corresponding nucleotide sugar is prepared by contacted the sialic acid derivative with an appropriate nucleotide triphosphates and a synthetase. The chloro group on the sialic acid moiety is then displaced with a nucleophilic PEG derivative, such as thio-PEG.

In a further exemplary embodiment, as shown is Scheme 6, a mannosamine is acylated with a bis-HOPT dicarboxylate, producing the corresponding amido-alkyl-carboxylic acid, which is subsequently converted to a sialic acid derivative. The sialic acid derivative is converted to a nucleotide sugar, and the carboxylic acid is activated and reacted with a nucleophilic PEG derivative, such as amino-PEG.
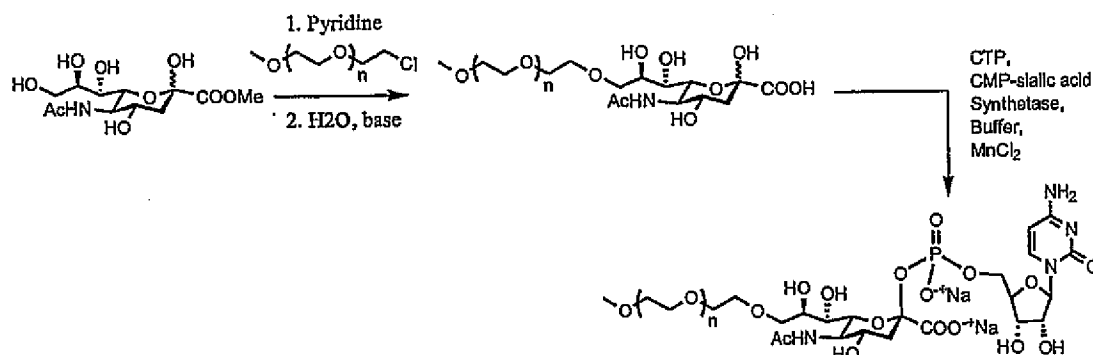
Scheme 6
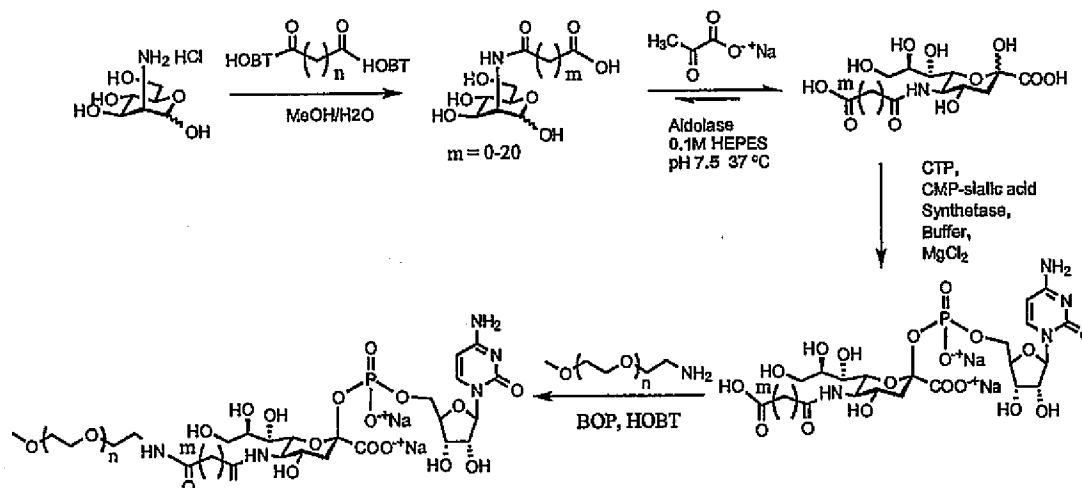
In another exemplary embodiment, set forth in Scheme 7, amine- and carboxyl-
protected neuraminic acid is activated by converting the primary hydroxyl group to the
corresponding p-toluenesulfonate ester, and the methyl ester is cleaved. The activated
neuraminic acid is converted to the corresponding nucleotide sugar, and the activating group
5   is displaced by a nucleophilic PEG species, such as thio-PEG.

Scheme 7
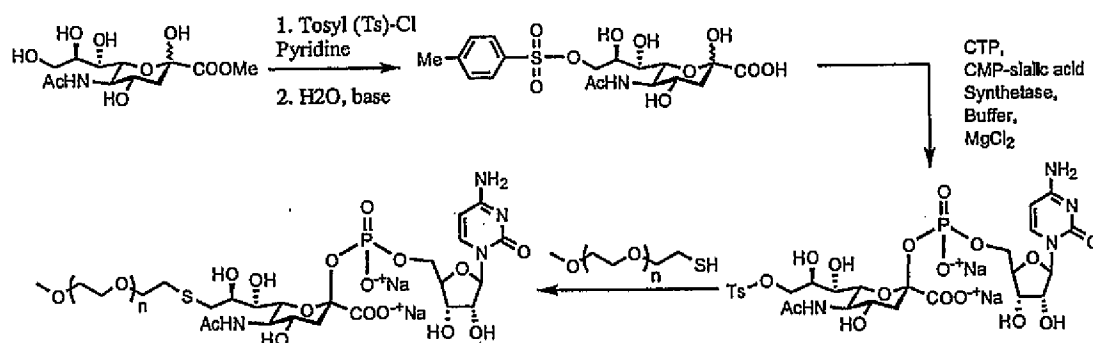
10   In yet a further exemplary embodiment, as set forth in Scheme 8, the primary
hydroxyl moiety of an amine- and carboxyl-protected neuraminic acid derivative is alkylated
using an electrophilic PEG, such as chloro-PEG. The methyl ester is subsequently cleaved
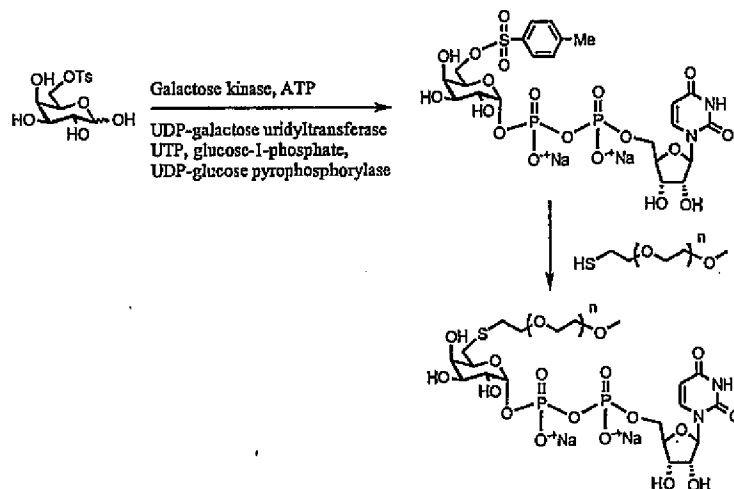and the PEG-sugar is converted to a nucleotide sugar.

15   **Scheme 8**

Glycans other than sialic acid can be derivatized with PEG using the methods set forth
herein. The derivatized glycans, themselves, are also within the scope of the invention.
20   Thus, Scheme 9 provides an exemplary synthetic route to a PEGylated galactose nucleotide

sugar. The primary hydroxyl group of galactose is activated as the corresponding toluenesulfonate ester, which is subsequently converted to a nucleotide sugar.
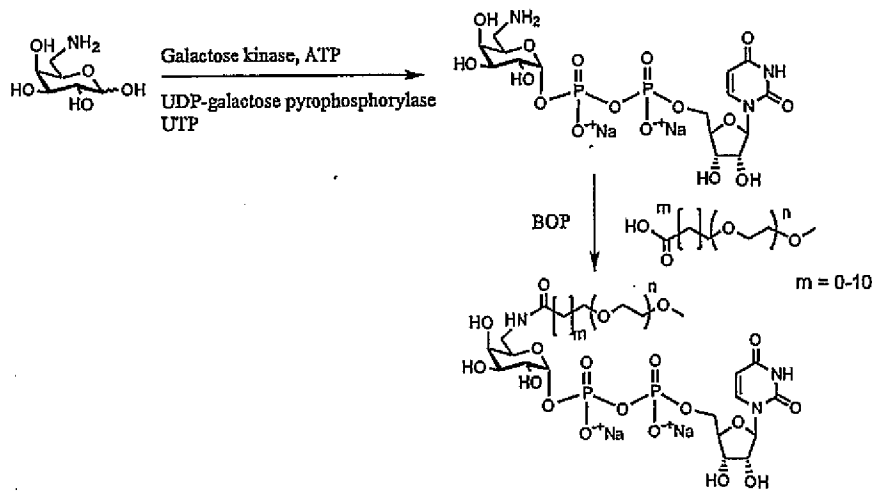
Scheme 9

5

Scheme 10 sets forth an exemplary route for preparing a galactose-PEG derivative that is based upon a galactose-6-amine moiety. Thus, galactosamine is converted to a nucleotide sugar, and the amine moiety of galactosamine is functionalized with an active

10   PEG derivative.

Scheme 10

AND DRUG DELIVERY SYSTEMS, ACS Symposium Series Vol. 469, American Chemical Society, Washington, D.C. 1991).

Purification of sugars, nucleotide sugars and derivatives

5   The nucleotide sugars and derivatives produced by the above processes can be used without purification. However, it is usually preferred to recover the product. Standard, well-known techniques for recovery of glycosylated saccharides such as thin or thick layer chromatography, column chromatography, ion exchange chromatography, or membrane filtration can be used. It is preferred to use membrane filtration, more preferably utilizing a reverse osmotic membrane, or one or more column chromatographic techniques for the

10   recovery as is discussed hereinafter and in the literature cited herein. For instance, membrane filtration wherein the membranes have molecular weight cutoff of about 3000 to about 10,000 can be used to remove proteins for reagents having a molecular weight of less than 10,000 Da.. Membrane filtration or reverse osmosis can then be used to remove salts and/or purify the product saccharides (see, e.g., WO 98/15581). Nanofilter membranes are a class of

15   reverse osmosis membranes that pass monovalent salts but retain polyvalent salts and uncharged solutes larger than about 100 to about 2,000 Daltons, depending upon the membrane used. Thus, in a typical application, saccharides prepared by the methods of the present invention will be retained in the membrane and contaminating salts will pass through.

20   ### G. Cross-linking Groups

Preparation of the modified sugar for use in the methods of the present invention includes attachment of a modifying group to a sugar residue and forming a stable adduct, which is a substrate for a glycosyltransferase. Thus, it is often preferred to use a cross-linking agent to conjugate the modifying group and the sugar. Exemplary bifunctional

25   compounds which can be used for attaching modifying groups to carbohydrate moieties include, but are not limited to, bifunctional poly(ethylene glycols), polyamides, polyethers, polyesters and the like. General approaches for linking carbohydrates to other molecules are known in the literature. See, for example, Lee et al., Biochemistry 28: 1856 (1989); Bhatia et al., Anal. Biochem. 178: 408 (1989); Janda et al., J. Am. Chem. Soc. 112: 8886 (1990) and

30   Bednarski et al., WO 92/18135. In the discussion that follows, the reactive groups are treated as benign on the sugar moiety of the nascent modified sugar. The focus of the discussion is

of the modified sugar to act as a glycosyltransferase substrate, crosslinkers can be used which introduce long spacer arms between components and include derivatives of some of the previously mentioned crosslinkers (*i.e.*, SPDP). Thus, there is an abundance of suitable crosslinkers, which are useful; each of which is selected depending on the effects it has on
5 optimal peptide conjugate and modified sugar production.

A variety of reagents are used to modify the components of the modified sugar with intramolecular chemical crosslinks (for reviews of crosslinking reagents and crosslinking procedures see: Wold, F., *Meth. Enzymol.* **25**: 623-651, 1972; Weetall, H. H., and Cooney, D. A., In: ENZYMES AS DRUGS. (Holcenberg, and Roberts, eds.) pp. 395-442, Wiley, New York,
10 1981; Ji, T. H., *Meth. Enzymol.* **91**: 580-609, 1983; Mattson *et al.*, *Mol. Biol. Rep.* **17**: 167-183, 1993, all of which are incorporated herein by reference). Preferred crosslinking reagents are derived from various zero-length, homo-bifunctional, and hetero-bifunctional crosslinking reagents. Zero-length crosslinking reagents include direct conjugation of two intrinsic chemical groups with no introduction of extrinsic material. Agents that catalyze formation of
15 a disulfide bond belong to this category. Another example is reagents that induce condensation of a carboxyl and a primary amino group to form an amide bond such as carbodiimides, ethylchloroformate, Woodward's reagent K (2-ethyl-5-phenylisoxazolium-3'-sulfonate), and carbonyldiimidazole. In addition to these chemical reagents, the enzyme transglutaminase (glutamyl-peptide γ-glutamyltransferase; EC 2.3.2.13) may be used as zero-
20 length crosslinking reagent. This enzyme catalyzes acyl transfer reactions at carboxamide groups of protein-bound glutaminyl residues, usually with a primary amino group as substrate. Preferred homo- and hetero-bifunctional reagents contain two identical or two dissimilar sites, respectively, which may be reactive for amino, sulfhydryl, guanidino, indole, or nonspecific groups.

25

2. Preferred Specific Sites in Crosslinking Reagents

a. Amino-Reactive Groups

In one preferred embodiment, the sites on the cross-linker are amino-reactive groups. Useful non-limiting examples of amino-reactive groups include N-hydroxysuccinimide
30 (NHS) esters, imidoesters, isocyanates, acylhalides, arylazides, p-nitrophenyl esters, aldehydes, and sulfonyl chlorides.

are stable, when conjugated to another double bond. The resonant interaction of both double bonds prevents hydrolysis of the Schiff linkage. Furthermore, amines at high local concentrations can attack the ethylenic double bond to form a stable Michael addition product.

5   Aromatic sulfonyl chlorides react with a variety of sites of the modified sugar components, but reaction with the amino groups is the most important, resulting in a stable sulfonamide linkage.

b. Sulfhydryl-Reactive Groups

10   In another preferred embodiment, the sites are sulfhydryl-reactive groups. Useful, non-limiting examples of sulfhydryl-reactive groups include maleimides, alkyl halides, pyridyl disulfides, and thiophthalimides.

Maleimides react preferentially with the sulfhydryl group of the modified sugar components to form stable thioether bonds. They also react at a much slower rate with

15   primary amino groups and the imidazole groups of histidines. However, at pH 7 the maleimide group can be considered a sulfhydryl-specific group, since at this pH the reaction rate of simple thiols is 1000-fold greater than that of the corresponding amine.

Alkyl halides react with sulfhydryl groups, sulfides, imidazoles, and amino groups. At neutral to slightly alkaline pH, however, alkyl halides react primarily with sulfhydryl

20   groups to form stable thioether bonds. At higher pH, reaction with amino groups is favored.

Pyridyl disulfides react with free sulfhydryls via disulfide exchange to give mixed disulfides. As a result, pyridyl disulfides are the most specific sulfhydryl-reactive groups.

Thiophthalimides react with free sulfhydryl groups to form disulfides.

c. Carboxyl-Reactive Residue

25

In another embodiment, carbodiimides soluble in both water and organic solvent, are used as carboxyl-reactive reagents. These compounds react with free carboxyl groups forming a pseudourea that can then coupled to available amines yielding an amide linkage. Procedures to modify a carboxyl group with carbodiimide is well know in the art (see,

30   Yamada *et al., Biochemistry* 20: 4836-4842, 1981).

methoxydiphenylmethane-4,4'-diisocyanate, 2,2'-dicarboxy-4,4'-azophenyldiisocyanate, and

hexamethylenediisocyanate.

Preferred, non-limiting examples of homobifunctional arylhalides include 1,5-

difluoro-2,4-dinitrobenzene (DFDNB), and 4,4'-difluoro-3,3'-dinitrophenyl-sulfone.

5   Preferred, non-limiting examples of homobifunctional aliphatic aldehyde reagents

include glyoxal, malondialdehyde, and glutaraldehyde.

Preferred, non-limiting examples of homobifunctional acylating reagents include

nitrophenyl esters of dicarboxylic acids.

Preferred, non-limiting examples of homobifunctional aromatic sulfonyl chlorides

10   include phenol-2,4-disulfonyl chloride, and α-naphthol-2,4-disulfonyl chloride.

Preferred, non-limiting examples of additional amino-reactive homobifunctional

reagents include erythritolbiscarbonate which reacts with amines to give biscarbamates.

b. Homobifunctional Crosslinkers Reactive with Free Sulfhydryl
15   Groups

Synthesis, properties, and applications of such reagents are described in the literature

(for reviews of crosslinking procedures and reagents, *see above*). Many of the reagents are

commercially available (*e.g.*, Pierce Chemical Company, Rockford, Ill.; Sigma Chemical

Company, St. Louis, Mo.; Molecular Probes, Inc., Eugene, OR).

20   Preferred, non-limiting examples of homobifunctional maleimides include

bismaleimidohexane (BMH), N,N'-(1,3-phenylene) bismaleimide, N,N'-(1,2-

phenylene)bismaleimide, azophenyldimaleimide, and bis(N-maleimidomethyl)ether.

Preferred, non-limiting examples of homobifunctional pyridyl disulfides include 1,4-

di-3'-(2'-pyridyldithio)propionamidobutane (DPDPB).

25   Preferred, non-limiting examples of homobifunctional alkyl halides include 2,2'-

dicarboxy-4,4'-diiodoacetamidoazobenzene, α,α'-diiodo-p-xylenesulfonic acid, α, α'-dibromo-

p-xylenesulfonic acid, N,N'-bis(b-bromoethyl)benzylamine, N,N'-

di(bromoacetyl)phenylthydrazine, and 1,2-di(bromoacetyl)amino-3-phenylpropane.

m-maleimidobenzoyl-N-hydroxysuccinimide ester (MBS), m-maleimidobenzoyl-N-hydroxysulfosuccinimide ester (sulfo-MBS), succinimidyl 4-(N-maleimidomethyl)-cyclohexane-1-carboxylate (SMCC), sulfosuccinimidyl 4-(N-maleimidomethyl)cyclohexane-1-carboxylate (sulfo-SMCC), succinimidyl 4-(p-maleimidophenyl)butyrate (SMPB), and

5   sulfosuccinimidyl 4-(p-maleimidophenyl)butyrate (sulfo-SMPB).

c. Amino-Reactive HeteroBifunctional Reagents with an Alkyl Halide Moiety

Synthesis, properties, and applications of such reagents are described in the literature.

10   Preferred, non-limiting examples of hetero-bifunctional reagents with an alkyl halide moiety and an amino-reactive NHS ester include N-succinimidyl-(4-iodoacetyl)aminobenzoate (SIAB), sulfosuccinimidyl-(4-iodoacetyl)aminobenzoate (sulfo-SIAB), succinimidyl-6-(iodoacetyl)aminohexanoate (SIAX), succinimidyl-6-(6-((iodoacetyl)-amino)hexanoylamino)hexanoate (SIAXX), succinimidyl-6-(((4-(iodoacetyl)-amino)-

15   methyl)-cyclohexane-1-carbonyl)aminohexanoate (SIACX), and succinimidyl-4((iodoacetyl)-amino)methylcyclohexane-1-carboxylate (SIAC).

A preferred example of a hetero-bifunctional reagent with an amino-reactive NHS ester and an alkyl dihalide moiety is N-hydroxysuccinimidyl 2,3-dibromopropionate (SDBP). SDBP introduces intramolecular crosslinks to the affinity component by conjugating its

20   amino groups. The reactivity of the dibromopropionyl moiety towards primary amine groups is controlled by the reaction temperature (McKenzie *et al., Protein Chem.* 7: 581-592 (1988)).

Preferred, non-limiting examples of hetero-bifunctional reagents with an alkyl halide moiety and an amino-reactive p-nitrophenyl ester moiety include p-nitrophenyl iodoacetate

25   (NPIA).

Other cross-linking agents are known to those of skill in the art. *See*, for example, Pomato *et al.*, U.S. Patent No. 5,965,106. It is within the abilities of one of skill in the art to choose an appropriate cross-linking agent for a particular application.

amount for a given enzyme under preselected substrate concentrations and reaction conditions are well known to those of skill in the art.

The temperature at which an above-described process is carried out can range from just above freezing to the temperature at which the most sensitive enzyme denatures.

5   Preferred temperature ranges are about 0 °C to about 55 °C, and more preferably about 30 °C to about 37 °C. In another exemplary embodiment, one or more components of the present method are conducted at an elevated temperature using a thermophilic enzyme.

The reaction mixture is maintained for a period of time sufficient for the acceptor to be glycosylated, thereby forming the desired conjugate. Some of the conjugate can often be

10 detected after a few hours, with recoverable amounts usually being obtained within 24 hours or less. Those of skill in the art understand that the rate of reaction is dependent on a number of variable factors (e.g, enzyme concentration, donor concentration, acceptor concentration, temperature, solvent volume), which are optimized for a selected system.

The present invention also provides for the industrial-scale production of modified

15 peptides. As used herein, an industrial scale generally produces at least one gram of finished, purified conjugate.

In the discussion that follows, the invention is exemplified by the conjugation of modified sialic acid moieties to a glycosylated peptide. The exemplary modified sialic acid is labeled with PEG. The focus of the following discussion on the use of PEG-modified sialic

20 acid and glycosylated peptides is for clarity of illustration and is not intended to imply that the invention is limited to the conjugation of these two partners. One of skill understands that the discussion is generally applicable to the additions of modified glycosyl moieties other than sialic acid. Moreover, the discussion is equally applicable to the modification of a glycosyl unit with agents other than PEG including other water-soluble polymers, therapeutic

25 moieties, and biomolecules.

An enzymatic approach can be used for the selective introduction of PEGylated or PPGylated carbohydrates onto a peptide or glycopeptide. The method utilizes modified sugars containing PEG, PPG, or a masked reactive functional group, and is combined with the appropriate glycosyltransferase or glycosynthase. By selecting the glycosyltransferase

30 that will make the desired carbohydrate linkage and utilizing the modified sugar as the donor substrate, the PEG or PPG can be introduced directly onto the peptide backbone, onto

polymer. Alternatively, an unmodified Gal is added to the GlcNAc, followed by the addition of a sialic acid modified with a water-soluble sugar. In yet a further example, the terminal GlcNAc is conjugated with Gal and the GlcNAc is subsequently fucosylated with a modified fucose bearing a water-soluble polymer.

5   Figure 16 is a scheme similar to that shown in Figure 13, in which high mannose is trimmed back to the first GlcNAc attached to the Asn of the peptide. In one example, the GlcNAc of the GlcNAc-(Fuc)$_a$ residue is conjugated with a GlcNAc bearing a water soluble polymer. In another example, the GlcNAc of the GlcNAc-(Fuc)$_a$ residue is modified with Gal, which bears a water soluble polymer. In a still further embodiment, the GlcNAc is
10   modified with Gal, followed by conjugation to the Gal of a sialic acid modified with a water-soluble polymer.

          Other exemplary embodiments are set forth in Figures 17-21. An illustration of the array of reaction types with which the present invention may be practiced is provided in each of the aforementioned figures.

.15   The Examples set forth above provide an illustration of the power of the methods set forth herein. Using the methods of the invention, it is possible to "trim back" and build up a carbohydrate residue of substantially any desired structure. The modified sugar can be added to the termini of the carbohydrate moiety as set forth above, or it can be intermediate between the peptide core and the terminus of the carbohydrate.

20   In an exemplary embodiment, an existing sialic acid is removed from a glycopeptide using a sialidase, thereby unmasking all or most of the underlying galactosyl residues. Alternatively, a peptide or glycopeptide is labeled with galactose residues, or an oligosaccharide residue that terminates in a galactose unit. Following the exposure of or addition of the galactose residues, an appropriate sialyltransferase is used to add a modified
25   sialic acid. The approach is summarized in Scheme 12.